

Kaushal
091734672 Page 1
Seq. IDs 1-3

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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:09:35 ; Search time 14037.5 Seconds

(without alignments)
11840.151 Million cell updates/sec

Title: US-09-734-672-1

Perfect score: 5711

Sequence: 1 AAGCTCGTGAAGACTTCTGTG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBankl:*

1: gb_ba:*

2: gb_hc:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_ov:*

7: gb_ph:*

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12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_or:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_scs:*

28: em_un:*

29: em_vl:*

30: em_hc: hum:*

31: em_hc: inv:*

32: em_hc: other:*

33: em_hc: mus:*

34: em_hc: pin:*

35: em_hc: rod:*

36: em_hc: mam:*

37: em_hc: vrt:*

38: em_sy:*

39: em_hcgo_hum:*

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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
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3	5711	100.0	5711	6	159546
4	5709.4	100.0	5711	6	AR007335
5	5709.4	100.0	5711	6	AR112809
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7	5701.4	99.8	5711	6	AR112810
8	5699.8	99.8	5711	6	AR033056
9	5699.8	99.8	5711	9	HS014680
10	5699.8	99.8	5712	6	AR070223
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12	5699.8	99.8	5712	6	AR125601
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ALIGNMENTS

RESULT 1

LOCUS AR007333 5711 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 1 from patent US 5750400.

ACCESSION AR007333

VERSION AR007333.1 GI:3966817

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 5711)

AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J., Scheller,D.B. and Zeng,B.

TITLE Coding sequences of the human BRCA1 gene

JOURNAL Patent: US 5750400-A 1 12-MAY-1998;

FEATURES
source
BASE COUNT 1953 a 1099 c 1277 g 1382 t
ORIGIN

Location/Qualifiers
1. 5711
/organism="unknown"

Query Match 100.0%; Score 5711; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AR112808
LOCUS AR112808 5711 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6130322.
ACCESSION AR112808
VERSION AR112808.1 GI:14092708
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,
Thurber, D., and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 6130322-A 1 10-OCT-2000;
FEATURES
source
1..5711
location/Qualifiers
BASE COUNT 1953 a 1099 c 1277 g 1382 t
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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181 TCTTAGAGTGTCCCATCTGTCTGAGAGTGTGATCAAGAACTGTCTCCAGAAAGTGTACC 240
181 TCTTAGAGTGTCCCATCTGTCTGAGAGTGTGATCAAGAACTGTCTCCAGAAAGTGTACC 240
241 ACAATTTTGGCAATTTTGGCATGCTGAAACTTCTCAACCAAGAAAGGCTTACAGT 300
241 ACAATTTTGGCAATTTTGGCATGCTGAAACTTCTCAACCAAGAAAGGCTTACAGT 300

Dh 241 ACAATATTTGCAAAATTTTGCATGCTGAAACTTCTCAACCAAGAAAGAGGCTTCAAGT 300
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Dh 301 GTTCCTTATGTAAGATGATATATACCAAAAGAGCTTACAAAGAAATGATGATATGATC 360
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Dh 601 CTGTGGAATCTGAGGACAAAGCAGCGGATACACTTCAAAAGAGCTGTCTACATG 660
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Dh 661 AATGAGGATCTGATTTCTTCTGAAAGATACCGTTAATAAGGCACTTTCAGAGTGGAG 720
Qy 721 ATCAAGAAATGTTACAAATCACCCCTCAAGAAACAGGAGTGAATCACTTTGATTCG 780
Dh 721 ATCAAGAAATGTTACAAATCACCCCTCAAGAAACAGGAGTGAATCACTTTGATTCG 780
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Dh 781 CAAAAAAGGCTGCTGTGAAATTTTCTGAGACCGATGTAACTCAATCTCAATCAAC 840
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Dh 841 CCAGTAATATGATTTGAAACACACTGAGAGGCTGAGTGAAGGCTTCCAGAAAGT 900
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Dh 1021 AAGGCTGAATTTCTGTATTAAGCAACAGCTGGCTTACAGAGGAGCCAACTAACAGT 1080
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Dh 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140
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Dh 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAAGATGAAATGAGCAAACTGCCATGCT 1200
Qy 1201 CAGAGATCTGAGATCTGAGAGATGTTCTTGTGATACCTAAATAGCAGATTTGAGA 1260
Dh 1201 CAGAGATCTGAGATCTGAGAGATGTTCTTGTGATACCTAAATAGCAGATTTGAGA 1260
Qy 1261 AAGTTAATGATGTTTTCAGAAAGTGAACCTGTTAGTTCGATGACTCAGATGATG 1320
Dh 1261 AAGTTAATGATGTTTTCAGAAAGTGAACCTGTTAGTTCGATGACTCAGATGATG 1320
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Dh 1321 GGGAGTCTGAATCAAAATGCAAAAGTGAAGTGTATTTGACGTTCTAAATGAGTATGATG 1380

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Dh 1621 AATTAAGGCTAAAGAGAGCCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680
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Dh 1681 CAGATTTGGCAGTCAAAAGAGCTCCTGAAATGATATATCAAGGAACTAAACAGGAGC 1740
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Dh 1741 AGAATGCTCAAGTGAATATATTAATATAGTGTCAATGAGATATTAACAAAGGATTT 1800
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTCGAAAAAGATCTGCTTCA 1860
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Qy 1861 AAAGGAAAGCTGAACTTAAAGCAGCAGTATTAAGAAATGAAATGAAATGAAATGAA 1920
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Dh 1981 ATGCGCTTGAATAGTATGATAGTAAATCTAAGCCCACTAATTTGATCTGAATTCGAA 2040
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Dh 2101 GGCACAGCAGAACTTCAACATGAGAAAGTAAAGAACTGCACTGAGGCAAGAAAG 2160
Qy 2161 GTTAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTATATCTTCCAGAGCTGA 2220
Dh 2161 GTTAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTATATCTTCCAGAGCTGA 2220
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Dh 2221 AGTTAAACAATGCACTGCTTCTTACTAAGTGTCAAAATACAGTGAATCTTAAGAT 2280
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Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAACTG 2400
Dh 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAACTG 2400
Qy 2401 AAAAGTCTGTAGAGTGAAGTGAATTTCACTGTGATCCTGTGATGATGCACTCAGG 2460
Dh 2401 AAAAGTCTGTAGAGTGAAGTGAATTTCACTGTGATCCTGTGATGATGCACTCAGG 2460

QY	2461	AAAGTATCTCGTACTCTGGAAGTTAGCACTTAGGAAAGCCAAAACAGAACCAATAAT	2520
Db	2461	AAAGTATCTCGTACTCTGGAAGTTAGCACTTAGGAAAGGCCAAAACAGAACCAATAAT	2520
QY	2521	GTGTGAGTCAGTGTGCAGCATTTGGAAAACCCCAAGGGACTAAATCATGGTGTTCAAAG	2580
Db	2521	GTGTGAGTCAGTGTGCAGCATTTGGAAAACCCCAAGGGACTAAATCATGGTGTTCCAAG	2580
QY	2581	ATPATGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC	2640
Db	2581	ATPATGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC	2640
QY	2641	GGGAAACAAAGCATGGAATGGAAAGAAAGTGAACCTTGATGCTCAGTATTTGGCAATACAT	2700
Db	2641	GGGAAACAAAGCATGGAATGGAAAGAAAGTGAACCTTGATGCTCAGTATTTGGCAATACAT	2700
QY	2701	TCMAAGTTTCAAAAGCCGACGTCATTTGCTCTGTTTCAAAATCCAGGAAATCCAGAAAGG	2760
Db	2701	TCMAAGTTTCAAAAGCCGACGTCATTTGCTCTGTTTCAAAATCCAGGAAATCCAGAAAGG	2760
QY	2761	AAATGTCACATTTCTGTCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AAATGTCACATTTCTGTCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
- QY	2821	TTGAATGTGACAAAGAAAGAAATCAAGAAAGAAATGACTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGACAAAGAAAGAAATCAAGAAAGAAATGACTCTTAATATCAAGCTGTAC	2880
- QY	2881	AGCAGTTTATATCACTGCAAGGCTTCTGTGGTGTGACGAAGATPAAGCAGTTGATA	2940
Db	2881	AGCAGTTTATATCACTGCAAGGCTTCTGTGGTGTGACGAAGATPAAGCAGTTGATA	2940
- QY	2941	ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
QY	3001	ACGAAACTGCACTCATTTACTCCAAATPAACATGACCTTTTCAAAACCCTATCTGTATAC	3060
Db	3001	ACGAAACTGCACTCATTTACTCCAAATPAACATGACCTTTTCAAAACCCTATCTGTATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCATTTGTTTAAATCTAATGTAAAGAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCATTTGTTTAAATCTAATGTAAAGAAATCTGCTAGAGG	3120
QY	3121	AAAACTTTGAGAAACATTCAATGTCACTGACCAAGAGAAATGGAAATGAGAAACATTCGA	3180
Db	3121	AAAACTTTGAGAAACATTCAATGTCACTGACCAAGAGAAATGGAAATGAGAAACATTCGA	3180
QY	3181	GTACAGTAGACCAATTAGCCGTATATACATTAGAGAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTAGACCAATTAGCCGTATATACATTAGAGAAATGTTTTTAAAGAGCCAGCT	3240
QY	3241	CAAGCAATTTAATGAAAGTAGTGTCCAGTACTAATGAAAGGGGCTCCAGATTAATGAA	3300
Db	3241	CAAGCAATTTAATGAAAGTAGTGTCCAGTACTAATGAAAGGGGCTCCAGATTAATGAA	3300
QY	3301	TAGGTTCCAGTGTGAAAAACATTCAACAGAACTAGGTAGAAACAGAGGGCCAAAATTTGA	3360
Db	3301	TAGGTTCCAGTGTGAAAAACATTCAACAGAACTAGGTAGAAACAGAGGGCCAAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATATAAACAAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATATAAACAAAGTCTTCTGGAA	3420
QY	3421	GTATTTGTAGCATCTCGAATAATAAAAAGCAAGATATGAAAGATGTGCTGAGCTGTA	3480
Db	3421	GTATTTGTAGCATCTCGAATAATAAAAAGCAAGATATGAAAGATGTGCTGAGCTGTA	3480
QY	3481	ATACAGATTTCTGCCATATCTGATTTCAAGTAACTTAGAAACAGCTATATGGGAAGTATGC	3540
Db	3481	ATACAGATTTCTGCCATATCTGATTTCAAGTAACTTAGAAACAGCTATATGGGAAGTATGC	3540
- QY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACTGTTAGATGATGTGAAATTAAGG	3600

Db	3541	ATGCATCTCAGGTTGTTCTGTGAGACCTGTGATGACCTTTGATGATGTGTAATAAAGG	3600
Oy	3601	AAGATACTAGTTTGTGCTGAAAAATGACATTAAGAAAGTTTGTGTTTAAAGCAAAACG	3660
Db	3601	AAGATACTAGTTTGTCTGAAAAATGCATTAAGAAAGTTGTGTTTAAAGCAAAACG	3660
Oy	3661	TCACAGAGGAGAGCTTTGACAGAGTCTAGCCCTTTAACCCATTCACATTTGGTCAAG	3720
Db	3661	TCACAGAGGAGAGCTTTGACAGAGTCTAGCCCTTTAACCCATTCACATTTGGTCAAG	3720
Oy	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCTCTCAAGAGAGAACTTACTAGTGAATG	3780
Db	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCTCTCAAGAGAGAACTTACTAGTGAATG	3780
Oy	3781	AAGAGCTTCCCTGCTTCCAAACCTTGTTATTTGGTAAATAAACATTAACCTTCCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACCTTGTTATTTGGTAAATAAACATTAACCTTCCAGT	3840
Oy	3841	CTACTAGGATATGACCCGTTGCTACCGAGTGTCTGTCTTAAGACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGATATGACCCGTTGCTACCGAGTGTCTGTCTTAAGACACAGAGAGAAATTTAT	3900
Oy	3901	TATCATTTAAGAAATGCTTAATATGATGCTGACATACACAGTAATATGGCAAAAGCATCTC	3960
Db	3901	TATCATTTAAGAAATGCTTAATATGATGCTGACATACACAGTAATATGGCAAAAGCATCTC	3960
Oy	3961	AGGACATCACCTTGTAGAGGAAACAAATGTCTGTAGCTTGTTTCTTACAGTGA	4020
Db	3961	AGGACATCACCTTGTAGAGGAAACAAATGTCTGTAGCTTGTTTCTTACAGTGA	4020
Oy	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGTCTTCTTGAATGGTCTT	4080
Db	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGTCTTCTTGAATGGTCTT	4080
Oy	4081	CCAAACAATAGAGCATAGTCTGAAACCCAGGGAGTGTCTGATGTACAAGGAATGG	4140
Db	4081	CCAAACAATAGAGCATAGTCTGAAACCCAGGGAGTGTCTGATGTACAAGGAATGG	4140
Oy	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATATTCAGAAAGCAAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATATATCAAGAAAGCAAAAGCA	4200
Oy	4201	TGGATTTCAAACCTTAGTGAAGACAGCATGTGGGTGTGAAGTGAAGAAACAGCTCTCTGAAG	4260
Db	4201	TGGATTTCAAACCTTAGTGAAGACAGCATGTGGGTGTGAAGTGAAGAAACAGCTCTCTGAAG	4260
Oy	4261	ACTGCTCAGGGGTATCTCTCTCAGATGACATTTTAAACCACTGAGAGGGATACCAATGC	4320
Db	4261	ACTGCTCAGGGGTATCTCTCTCAGATGACATTTTAAACCACTGAGAGGGATACCAATGC	4320
Oy	4321	AACATTAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAAGAGCTGTATTAGAACAGC	4380
Db	4321	AACATTAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAAGAGCTGTATTAGAACAGC	4380
Oy	4381	ATGGAGGACAGGCTTTTAAACAGCTAACCTTCCATCATTAAGTACTCTCTGCTTGAAG	4440
Db	4381	ATGGAGGACAGGCTTTTAAACAGCTAACCTTCCATCATTAAGTACTCTCTGCTTGAAG	4440
Oy	4441	ACCTGCGAAATCCAGAACAAAGCACAATCAGAAAAAGCAGTATTTAATTCAACAGAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCACAATCAGAAAAAGCAGTATTTAATTCAACAGAAAGTA	4500
Oy	4501	GTGAATTAACCTATTAAGCCAGAAATCCAGAAAGGCTTTTCGTGACAGCAAGTTTAGGGTGTG	4560
Db	4501	GTGAATTAACCTATTAAGCCAGAAATCCAGAAAGGCTTTTCGTGACAGCAAGTTTAGGGTGTG	4560
Oy	4561	CAGATAGTTCTACACAGTAAAAATTAAGAACCAAGAGGTGGAAGGTCATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTACACAGTAAAAATTAAGAACCAAGAGGTGGAAGGTCATCCCTCTTAAT	4620
Oy	4621	GCCCATCATTAAGATATAGTGTGATCATGCAAGTTGCTTGGAGTCTTCAGAAATAGAA	4680
Db	4621	GCCCATCATTAAGATATAGTGTGATCATGCAAGTTGCTTGGAGTCTTCAGAAATAGAA	4680

Db 4621 GCCCATCATTAGATGATAGTGTGATGACATGCACAGTTGCTCTGGAGCTTTCAGAAATAGAA 4680
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Db 4681 ACTACCATCTCAAGAGAGAGCTCATTAGGTTGTATGATGAGAGCAACAGCTGAAG 4740
Qy 4741 AGTCTGGGCAACAGATTTGACGGAAACATCTTACTTCTGCAAGAGCAAGATCTAGAGGAA 4800
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Db 4801 CCCCTTACTGGAATCTGGAATAGCCTCTCTCTGATGACCTGATCTGATCTCTG 4860
Qy 4861 AAGACAGAGCCGAGAGTACGCTGCTGAGCAACATTCATCTTCAACCTCTGATTA 4920
Db 4861 AAGACAGAGCCGAGAGTACGCTGCTGAGCAACATTCATCTTCAACCTCTGATTA 4920
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Db 4921 AAGTCCCAATGAAAGTTGACAAATCTGCCCCAGGCTCAGCTGCTGATCTACTATG 4980
Qy 4981 ATACTCTGGGTATATGCAATGGAAGAAAGTGTGACAGGAGCAAGCAAGATTTGACAG 5040
Db 4981 ATACTCTGGGTATATGCAATGGAAGAAAGTGTGACAGGAGCAAGCAAGATTTGACAG 5040
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Db 5101 AATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160
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Db 5581 TCCATGCAATTTGGGAGATGTGTGAGAGCCTGTGTGAGAGAGTGGGTGGAGAA 5640
Qy 5641 GTGTAGACTCTTACAGATGCTGAGAGAGCTGAGACCTTACTGATACCCAGATCTCCCA 5700
Db 5641 GTGTAGACTCTTACAGATGCTGAGAGAGCTGAGACCTTACTGATACCCAGATCTCCCA 5700
Qy 5701 GGCACCTACTGA 5711
Db 5701 GGCACCTACTGA 5711

RESULT 3
LOCUS 159546 5711 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5654155.
ACCESSION 159546
VERSION 159546.1 GI:2478178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvarez, C.P., Critz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.
TITLE Consensus sequence of the human BRCA1 gene
JOURNAL Patent: US 5654155-A 1 05-AUG-1997;
FEATURES
source location/Qualifiers
1..5711
BASE COUNT 1953 a 1099 c 1277 g 1382 t
ORIGIN
Query Match 100.0%; Score 5711; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCTGGCTGAGACTTCTCTGAGACCCCGCACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60
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Qy 61 CTGGGCTCAGAGAGGCTTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
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Qy 361 AACTTTGTAAGAGCTATTTGAAATCATTTTGTGCTTTTCAAGTGTACACAGGTTGGAGT 420
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Db 481 AAGTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGAGCTTCTACAGAGTG 540
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Qy 601 CTGTAGAACTCTGAGAGCAAGAGGAGATACAACTTCAAAAGAGCTGTGCTACATTG 660
Db 601 CTGTAGAACTCTGAGAGCAAGAGGAGATACAACTTCAAAAGAGCTGTGCTACATTG 660
Qy 661 AATTGGATCTGATTTCTTGAAGATACCTTAATTAAGCAACTTATTTAGTGTGGAG 720
Db 661 AATTGGATCTGATTTCTTGAAGATACCTTAATTAAGCAACTTATTTAGTGTGGAG 720

Db 661 AATTGGGATCTGATTTCTCTGAGATACCGTTAATAGGCACTTATTGCACTGTGGGAG 720
Qy 721 ATCAAGATTGTATCAAAATCACCCCTCAAGGACCAAGGATGAATCACTTTGGATTCTG 780
Db 721 ATCAAGATTGTATCAAAATCACCCCTCAAGGACCAAGGATGAATCACTTTGGATTCTG 780
Qy 781 CAAAAAGGCTGCTGTGATTTTCTGAGAGGATGTAACAAATCTGAAACATCATCAAC 840
Db 781 CAAAAAGGCTGCTGTGATTTTCTGAGAGGATGTAACAAATCTGAAACATCATCAAC 840
Qy 841 CCAGTAATTAATGATTTGGAACACCACTGAGAACCGTGCAGCTGAGAGGCATCCAGAAAGT 900
Db 841 CCAGTAATTAATGATTTGGAACACCACTGAGAACCGTGCAGCTGAGAGGCATCCAGAAAGT 900
Qy 901 ATCAGGAGTCTTCTGTTTCAAACTTGCACTGTGAGACCATGTGSCAAATCTCATGTCCA 960
Db 901 ATCAGGAGTCTTCTGTTTCAAACTTGCACTGTGAGACCATGTGSCAAATCTCATGTCCA 960
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Qy 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGCTGCTAGCAAGAGCCAACTAAACAGAT 1080
Db 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGCTGCTAGCAAGAGCCAACTAAACAGAT 1080
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Db 1081 GGGCTGGAAGTAAAGAAACATGTATATAGGCGGATCTCCAGCAGAGAAAAAGGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAAGAGAAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAAGAGAAACTGCCATGCT 1200
Qy 1201 CAGAGAACTCTAGAGATCTAGAGAGTGTCTTGATTAACACTAATAGCAGCATTTGAGA 1260
Db 1201 CAGAGAACTCTAGAGATCTAGAGAGTGTCTTGATTAACACTAATAGCAGCATTTGAGA 1260
Qy 1261 AAGTTAATGATGTTTTTCCAGAAAGTGAATCTTTAGCTTCTGATGACTCACTAGATG 1320
Db 1261 AAGTTAATGATGTTTTTCCAGAAAGTGAATCTTTAGCTTCTGATGACTCACTAGATG 1320
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGAGCGTTTAAATGAGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGAGCGTTTAAATGAGTAGATG 1380
Qy 1381 AATATTTCTGTTCTTCAAGAAATAGACTTACTGCGCAGTATCTCATGAGGCTTTAA 1440
Db 1381 AATATTTCTGTTCTTCAAGAAATAGACTTACTGCGCAGTATCTCATGAGGCTTTAA 1440
Qy 1441 TATGTTAAAGTGAAGAGTTCATCTCAATCAGTAGAGTAAATTTGAAAGCAAAATAT 1500
Db 1441 TATGTTAAAGTGAAGAGTTCATCTCAATCAGTAGAGTAAATTTGAAAGCAAAATAT 1500
Qy 1501 TTGGGAAAACCTATCGAAGAGGAGCAGCTCCCAACTTAAGCCATGTAACTGAAAATC 1560
Db 1501 TTGGGAAAACCTATCGAAGAGGAGCAGCTCCCAACTTAAGCCATGTAACTGAAAATC 1560
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Db 1621 AATTAAGGCTTAAGAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680
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Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTGGAATGATTAATCAAGGAACTAAACAGAGAC 1740
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Db 1741 AGAATGGTCAAGTGAATATTAATTAATAGTGTGATGAGAAATAAACAAAAGGTGATT 1800

Qy 1801 CTATTCAGAAATGAGAAAAATCCTAACCCAAATAGAAATGACTCGAAAAAGAAATCTGCTTCA 1860
Db 1801 CTATTCAGAAATGAGAAAAATCCTAACCCAAATAGAAATGACTCGAAAAAGAAATCTGCTTCA 1860
Qy 1861 AAAGCAAGCTGAAACCTTAAGACAGATATAGCAATATGGAATCTGAAATTAATATCC 1920
Db 1861 AAAGCAAGCTGAAACCTTAAGACAGATATAGCAATATGGAATCTGAAATTAATATCC 1920
Qy 1921 ACAATTCAAAAGCACCTTAAGAAATAGGCTGAGAGAGAACTCTTCAACAGCATATTC 1980
Db 1921 ACAATTCAAAAGCACCTTAAGAAATAGGCTGAGAGAGAACTCTTCAACAGCATATTC 1980
Qy 1981 ATGGGCTTGAACCTGTATGCTAGTAAATCTAACCCCACTAATTTAGTGAATTTGCAA 2040
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Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTATCAACCAATGCGAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTATCAACCAATGCGAGTCA 2100
Qy 2101 GGCACAGCAAAACCTTACAACTCATGGAAGGTAAAGAACTCTGCAACTGAGCCCAAGAGA 2160
Db 2101 GGCACAGCAAAACCTTACAACTCATGGAAGGTAAAGAACTCTGCAACTGAGCCCAAGAGA 2160
Qy 2161 GTAACCAAGCCAAATGAAACAGACAAATGAAGACATGACAGTATCTTCCAGAGCTGA 2220
Db 2161 GTAACCAAGCCAAATGAAACAGACAAATGAAGACATGACAGTATCTTCCAGAGCTGA 2220
Qy 2221 AGTTAACCAATGACACCTGGTTCTTTTACTAAGTGTCAAAATACCAAGTAACTTAAGAAAT 2280
Db 2221 AGTTAACCAATGACACCTGGTTCTTTTACTAAGTGTCAAAATACCAAGTAACTTAAGAAAT 2280
Qy 2281 TTGTCAATCTTACGCTTCCAAAGAGAAAGAAAGAAAGAACTGAAACGTTTAAAGTGT 2340
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Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTGTAAGTCTGATTAATGGAACCTGAG 2460
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Db 2521 GTGTGAGTCAAGTGTGAGCACTTTGAAAAACCCAGAGGACTAATCATGTTGTTCCAAAG 2580
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Db 2701 TCAAGGTTTCAAAAGGCGCAGTCACTTTGCTCTGTTTCAAAATCCAGAAATGAGAGAGG 2760
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Db 2761 AATGTGCAAACTTCTGCCCCACTCTGGGTCCTTTAAAGAAACAAAGTCAAAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAAGGAGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAAGGAGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCTGTAC 2880

QY	2881	AGACGTTAATATCACTGACGGCTTCTCTGCTGGTGGTCAGAAAAGTAAAGCACTGTTGATA	2940
Db	2881	AGACGTTAATATCACTGACGGCTTCTCTGCTGGTGGTCAGAAAAGTAAAGCACTGTTGATA	2940
QY	2941	ATGCCAAATGTGTATCAAAAGAGGCTCAGGTTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTGTATCAAAAGAGGCTCAGGTTTTGTCTATCATCTCAGTTCAGAGGCA	3000
QY	3001	ACGAAACTGCACTCACTTACTCCAAATTAACAATGACCTTTTACAAAAACCCATATGTTATAC	3060
Db	3001	ACGAAACTGCACTCACTTACTCCAAATTAACAATGACCTTTTACAAAAACCCATATGTTATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCATTTGTTAAAACTAAATGTAAAGAAAATCTGCTAAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCATTTGTTAAAACTAAATGTAAAGAAAATCTGCTAAGG	3120
QY	3121	AAAACCTTGGAGAACATTCATATGTCACCTGAAAAGAAATGGAAAATGAGAACATTCGAA	3180
Db	3121	AAAACCTTGGAGAACATTCATATGTCACCTGAAAAGAAATGGAAAATGAGAACATTCGAA	3180
QY	3181	GTACAGTAGACCAATTTAGCCGTAAATACATTAGAGAAAATGTTTTTAAAGACCACGCT	3240
Db	3181	GTACAGTAGACCAATTTAGCCGTAAATACATTAGAGAAAATGTTTTTAAAGACCACGCT	3240
QY	3241	CAGCAATATTATAGAGTAGGTTCCAGTACTAATGAATGGGCTCCAGATTTAATGAAA	3300
Db	3241	CAGCAATATTATAGAGTAGGTTCCAGTACTAATGAATGGGCTCCAGATTTAATGAAA	3300
QY	3301	TAGGTTCCAGTATGATAAAACATTCAAGCAGAACTATGTAAGAAACAGAGGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGATAAAACATTCAAGCAGAACTATGTAAGAAACAGAGGGCCAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGGCAACCTGAGGCTTATPAAACAAAGCTTCCTGAAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGGCAACCTGAGGCTTATPAAACAAAGCTTCCTGAAA	3420
QY	3421	GTAATGTGAAGCATCTGAAAAATAAAAAAGCAAGATATGAAGAAATGATTCAGACTGTA	3480
Db	3421	GTAATGTGAAGCATCTGAAAAATAAAAAAGCAAGATATGAAGAAATGATTCAGACTGTA	3480
QY	3481	ATACGATTTTCTCTCCATATCTGATTTAGATTAATTAGAACAGGCTATGGGAAATGCTC	3540
Db	3481	ATACGATTTTCTCTCCATATCTGATTTAGATTAATTAGAACAGGCTATGGGAAATGCTC	3540
QY	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTGTAGATGATGGTAAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTGTAGATGATGGTAAATTAAGG	3600
QY	3601	AAGATACTAGTTTGTCTGAAAAATGACATTAAGAGAAAGTTCTGCTGTTTTAGCAAAAACG	3660
Db	3601	AAGATACTAGTTTGTCTGAAAAATGACATTAAGAGAAAGTTCTGCTGTTTTAGCAAAAACG	3660
QY	3661	TCCAGAGAGGAGAGTTTGCAGAGAGTCTTAGCCCTTTTACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGGAGAGTTTGCAGAGAGTCTTAGCCCTTTTACCCATACACATTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAAGAAAGAACTTATCTAGTAGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAAGAAAGAACTTATCTAGTAGAGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCACACATTTGTATTTGGTAAAGTAAACATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACACATTTGTATTTGGTAAAGTAAACATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGACCCGCTTGCTACCGAGTCTGTCTTAAGAACACAGAGAGCAATTTAT	3900
Db	3841	CTACTAGGCATAGACCCGCTTGCTACCGAGTCTGTCTTAAGAACACAGAGAGCAATTTAT	3900
QY	3901	TATCATTAAGAAATGTGCTTAATATGCTGCACTAACCAAGTAAATATGTGGCAAAAGCACTC	3960
Db	3901	TATCATTAAGAAATGTGCTTAATATGCTGCACTAACCAAGTAAATATGTGGCAAAAGCACTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGAAACAAATATTTCTGATGCTGTTTTCTTCACATGCA	4020

Db	3961	AGGAACATCACCTTAGTAGAGAAA	CAAAATGTTCTGTAGAGTTGTTTCTTCA	CAGTGCA	4020	
Qy	4021	GTGAATTTGAAAGACTTGACTGCA	ATAAACCACCCAGAGATCCCTTCT	TGATTTGGTCTT	4080	
Db	4021	GTGAATTTGAAAGACTTGACTGCA	ATAAACCACCCAGAGATCCCTTCT	TGATTTGGTCTT	4080	
Qy	4081	CCAAACAAATGAGGATAGTCTGA	AAAGCCGAGGAGTTGGTCTG	AGTACAAAGAAATTGG	4140	
Db	4081	CCAAACAAATGAGGATAGTCTGA	AAAGCCGAGGAGTTGGTCTG	AGTACAAAGAAATTGG	4140	
Qy	4141	TTTCAGATGATGAAGAAAGAGAA	CGGGCTTGGAAAGAAATTAATCA	AGAAAGCAAGCA	4200	
Db	4141	TTTCAGATGATGAAGAAAGAGAA	CGGGCTTGGAAAGAAATTAATCA	AGAAAGCAAGCA	4200	
Qy	4201	TGGAATTCAAACTTGGTGAAGCA	CACATCTGGGGTGTGAGAGTGA	AAACAGCTCTCTGAG	4260	
Db	4201	TGGAATTCAAACTTGGTGAAGCA	CACATCTGGGGTGTGAGAGTGA	AAACAGCTCTCTGAG	4260	
Qy	4261	ACTGCTCAGGGCTATCCCTCT	CAGAGTGACATTTTAAACCACT	CACAGAGGATACATGC	4320	
Db	4261	ACTGCTCAGGGCTATCCCTCT	CAGAGTGACATTTTAAACCACT	CACAGAGGATACATGC	4320	
Qy	4321	AACATTAACCTGATTAAGCTCC	AGCAGAGAAATGGCTGAAC	CTGAAGCTGTGTTAAGACAGC	4380	
Db	4321	AACATTAACCTGATTAAGCTCC	AGCAGAGAAATGGCTGAAC	CTGAAGCTGTGTTAAGACAGC	4380	
Qy	4381	ATGGAGGACACCCCTTTPAAC	GCATACCTTCATATTAAGTACT	CTCTTGGCCCTTGAG	4440	
Db	4381	ATGGAGGACACCCCTTTPAAC	GCATACCTTCATATTAAGTACT	CTCTTGGCCCTTGAG	4440	
Qy	4441	ACCTGCGAAATCCAGAA	CAAGACATCAGAAAAAGCAGT	TTTAACCTTCA	CAGAAAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAA	CAAGACATCAGAAAAAGCAGT	TTTAACCTTCA	CAGAAAAAGTA	4500
Qy	4501	GTGAATACCTTATTAAGCC	AGATCCAGAGGCTTTTCTGT	GACAAAGTTGAGGTCTG	4560	
Db	4501	GTGAATACCTTATTAAGCC	AGATCCAGAGGCTTTTCTGT	GACAAAGTTGAGGTCTG	4560	
Qy	4561	CAGATAGTTCACCAAGTAA	ATAAAGAACAGAGTGGAAAG	GTCAATCCCTCTTAAT	4620	
Db	4561	CAGATAGTTCACCAAGTAA	ATAAAGAACAGAGTGGAAAG	GTCAATCCCTCTTAAT	4620	
Qy	4621	GCCCATCTTATGATGATAGT	AGTGTATACATG	CACAGTGGAGTCTT	CAGAAATGAA	4680
Db	4621	GCCCATCTTATGATGATAGT	AGTGTATACATG	CACAGTGGAGTCTT	CAGAAATGAA	4680
Qy	4681	ACTAACCATCTCAAGAGAG	CTCATTAAGTGTGTA	TGTGAGAGAGCA	CAGCTGGAAG	4740
Db	4681	ACTAACCATCTCAAGAGAG	CTCATTAAGTGTGTA	TGTGAGAGAGCA	CAGCTGGAAG	4740
Qy	4741	AGTCTGGGCCACACAGAT	TTTGAACGAAATCTTAC	CGCAAGCAATTTA	AGGGAA	4800
Db	4741	AGTCTGGGCCACACAGAT	TTTGAACGAAATCTTAC	CGCAAGCAATTTA	AGGGAA	4800
Qy	4801	CCCCCTTACCTGGAATCTG	GAATCAAGCTCTTCTG	ATGACCTTGAATCTG	ATCTTCTG	4860
Db	4801	CCCCCTTACCTGGAATCTG	GAATCAAGCTCTTCTG	ATGACCTTGAATCTG	ATCTTCTG	4860
Qy	4861	AAGAAGAGCCCAAGAGTCA	AGCTGTGTGGCA	CATACATCTTCA	ACCTCTGATTTGA	4920
Db	4861	AAGAAGAGCCCAAGAGTCA	AGCTGTGTGGCA	CATACATCTTCA	ACCTCTGATTTGA	4920
Qy	4921	AAAGTTCCCAATTAAGAT	TGACAAATCTGCCAGGGT	CCAGCTGCTCATTA	CTACTG	4980
Db	4921	AAAGTTCCCAATTAAGAT	TGACAAATCTGCCAGGGT	CCAGCTGCTCATTA	CTACTG	4980
Qy	4981	ATTACTGCTGGGTATTAAT	GCAATGGAAGAAAGTGTGA	CACAGGAGAAAGC	AGAAATTTGACAG	5040
Db	4981	ATTACTGCTGGGTATTAAT	GCAATGGAAGAAAGTGTGA	CACAGGAGAAAGC	AGAAATTTGACAG	5040
Qy	5041	CTTCAACAGAAAGGATCA	CAAAAGAAATGTCAT	GTGTGTGCTGAGCTG	CAACCCCAAG	5100

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AR007335 5711 bp DNA linear PAT 04-DEC-1998
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DEFINITION Sequence 5 from patent US 5750400.
ACCESSION AR007335
VERSION AR007335.1 GI:3966819
KEYWORDS
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 5750400-A 5 12-MAY-1998;
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BASE COUNT 1953 a 1098 c 1277 g 1383 t
ORIGIN
Query Match 100.0%; Score 5709.4; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION AR112809
VERSION AR112809.1 GI:14092709
KEYWORDS
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Crlitz, B.S., Olson, S.J.,
Thurber, D. and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 6130322-A 3 10-OCT-2000;
FEATURES
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Query Match 100.0%; Score 5709.4; DB 6; Length 5711;
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Unclassified.
1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Citz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 5750400-A 3 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..5711
/organism="unknown"
BASE COUNT 1956 a 1098 c 1274 g 1383 t
ORIGIN
Query Match 99.8%; Score 5701.4; DB 6; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 1921 ACAATTCAAAAGCACTTAAGAAATAGCTGAGAGAAAGCTTTTCAACAGGCAATATTC 1980

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Db	1981	ATGCGCTTGAACCTAGTAGTCAGTAGAAATCTPAAGCCCACTPAATTGTACTAAATTGCCAA	2040
QY	2041	TTGATAGTGTCTCTAGCACTGTAAGGATTAAGAAAAAAAAGTATACCAATATGCACTCA	2100
Db	2041	TTGATAGTGTCTCTAGCACTGTAAGGATTAAGAAAAAAAAGTATACCAATATGCACTCA	2100
QY	2101	GGCAGAGAGAAAACCTTACAACCTCATGAGAAAGTTAAAAAAGCTGCAACTGAGACCAGAA	2160
Db	2101	GGCAGAGAGAAAACCTTACAACCTCATGAGAAAGTTAAAAAAGCTGCAACTGAGACCAGAA	2160
QY	2161	GTAACAAGCCAAATGAAACAGACAAAGTAAAGACATGACAGGATATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAAACAGACAAAGTAAAGACATGACAGGATATCTTTCCAGAGCTGA	2220
QY	2221	AGTTAAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATCCAGTGAATCTTAAAGAT	2280
Db	2221	AGTTAAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAAATCCAGTGAATCTTAAAGAT	2280
QY	2281	TTGTCAATCTAGACCTTCCAGAGAAAAGAAAGAGAAACCTGAAACATTTAAAGGT	2340
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QY	2401	AAAGATCTGTAGAGATGACAGTATTTCACTGTGTACTGTACTGATTTATGGCACTAAG	2460
Db	2401	AAAGATCTGTAGAGATGACAGTATTTCACTGTGTACTGTACTGATTTATGGCACTAAG	2460
QY	2461	AAAGATCTGCTTACTGGAAGTTGCACTTAGGGAGGCAAAAACGAACCAATTAAT	2520
Db	2461	AAAGATCTGCTTACTGGAAGTTGCACTTAGGGAGGCAAAAACGAACCAATTAAT	2520
QY	2521	GTGTAGTCAGTGTGACAGACTTTGAAAAACCCCAAGGAGCTAATTCAATGTTGTTCCAAG	2580
Db	2521	GTGTAGTCAGTGTGACAGACTTTGAAAAACCCCAAGGAGCTAATTCAATGTTGTTCCAAG	2580
QY	2581	ATATATGAATGACACAGAGGCTTTAATATCAATTGGGACATGAAGTTAACACAGTC	2640
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Db	2641	GGGAACAAGCAATGGAATGGAAGAAAGTGAACCTTAATGCTCAATTTTGGAGAAATCAT	2700
QY	2701	TCAAGGTTTCAAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGAGAAATCAGAAAGG	2760
Db	2701	TCAAGGTTTCAAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGAGAAATCAGAAAGG	2760
QY	2761	AATGTGCAAACTTCTCTGCGCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAAACTTCTCTGCGCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGAATGTGAACAAAAGAGAAATAACAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
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QY	2941	ATGCCAAATGATATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
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QY	3001	ACGAATCTGAGTCACTTCTCTCAATTAACATGACCTTTTACAAAACCCCATATGTATAC	3060
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QY	3061	CACACCTTTTCCCATCAAGCACTTGGTTAAATCAATATGTAAGAAATCTGCTAGAG	3122
Db	3061	CACCACTTTTCCCATCAAGCACTTGGTTAAATCAATATGTAAGAAATCTGCTAGAG	3122
QY	3121	AAAACTTTAGAGAACTTCAATGTCACCTGAAGAGAAATGGAAATGAGAACTTCCAA	3180
Db	3121	AAACTTTAGAGAACTTCAATGTCACCTGAAGAGAAATGGAAATGAGAACTTCCAA	3180
QY	3181	GTACAGTAGACAATTAAGAGTAAATCACTTAAGAGAAATGCTTTTAAAGAGCAAGCT	3240
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QY	3361	ATGCAATCTTAAATTAAGGGGTTTGGCACTGAGAGCTATTAACAAAGCTTCTCTGGAA	3420
Db	3361	ATGCAATCTTAAATTAAGGGGTTTGGCACTGAGAGCTATTAACAAAGCTTCTCTGGAA	3420
QY	3421	GTAATTGTAGACATCTCGAAATTAACAAAGCAGAAATAGAAAGTAGATTGACACTGTTA	3480
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QY	3481	ATACAGATTTTCTTCCATATCTGATTTCAATTAATTAGAACACGCTTATGGGAAGTAGTC	3540
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ACCESSION AR112810
VERSION AR112810.1 GI:14092710
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Citz, B.S., Olson, S.J.,
Thurber, P.D. and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 6130322-A 5 10-OCT-2000;
FEATURES
source location/Qualifiers
1..5711
/organism="unknown"
BASE COUNT 1956 a 1098 c 1274 g 1383 t
ORIGIN.

Query Match 99.8%; Score 5701.4; DB 6; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
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121 TGGATTTATCTGCTTCTGCTGCTTGAAGAGTAAATGTCATTAATGCTATGAGAAA 180
121 TGGATTTATCTGCTTCTGCTGCTTGAAGAGTAAATGTCATTAATGCTATGAGAAA 180

QY 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGGAACCTGTCTCCAAAGTGAGCC 240
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGGAACCTGTCTCCAAAGTGAGCC 240
QY 241 ACATATTTTGCATTTTGCATGCTGAACCTTCTCAACCAAGAAAGGGCTTTCACAGT 300
Db 241 ACATATTTTGCATTTTGCATGCTGAACCTTCTCAACCAAGAAAGGGCTTTCACAGT 300
QY 301 GTCTTTATGTAAAGATATTAACCAAAAGAGCCCTACAAAGAAAGTATTAAGT 360
Db 301 GTCTTTATGTAAAGATATTAACCAAAAGAGCCCTACAAAGAAAGTATTAAGT 360
QY 361 AACTTGTGAAGCTATTTGAAAATCATTTGTGCTTTTCAGCTTGAACAGAGTTTGAAGT 420
Db 361 AACTTGTGAAGCTATTTGAAAATCATTTGTGCTTTTCAGCTTGAACAGAGTTTGAAGT 420
QY 421 ATGCAAAACAGCTATTAATTTTGCATTTTGCATTTTGCATTTTGCATTTTGCATTT 480
Db 421 ATGCAAAACAGCTATTAATTTTGCATTTTGCATTTTGCATTTTGCATTTTGCATTT 480
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Db 481 AAGTTCTATCATCAAAAGATGAGGCTACAGAAAACCGTCCAAAAGACTTCTACAGAGT 540
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Db 661 AATTGGAGTGTGATCTTCTGAGAGATCCGTATTAAGGCACTTATTCAGTGTGAG 720
QY 721 ATCAAGAAATTTGTAACAATCAACCCCTCAAGGAAACAGGATGAATCAGTTTGAATCTG 780
Db 721 ATCAAGAAATTTGTAACAATCAACCCCTCAAGGAAACAGGATGAATCAGTTTGAATCTG 780
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Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840
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Db 841 CCAGTATATATGATTTGAACCACTGAGAGGCTGAGTGAAGGCAATCCAGAAAGT 900
QY 901 ATCAGGATAGTTCCTGTTTCAAACTTGATGTGAGGCAATCTCATGCA 960
Db 901 ATCAGGATAGTTCCTGTTTCAAACTTGATGTGAGGCAATCTCATGCA 960
QY 961 GCTCATTTACAGATGAGACAGATTTTATCTCACTAAAGACAGATGATGAGAA 1020
Db 961 GCTCATTTACAGATGAGACAGATTTTATCTCACTAAAGACAGATGATGAGAA 1020
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Db 1021 AGGCTGAATTTCTGTAATTAAGCAAGCGCTGCTTGAAGAGGCAATTAAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGACCTCCAGCAAGAAAAGAGT 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGACCTCCAGCAAGAAAAGAGT 1140
QY 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGAATTAAGCAAGAACTGCTGCT 1200
Db 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGAATTAAGCAAGAACTGCTGCT 1200
QY 1201 CAGAGATCTTAGAGTACTGAGATGTTTCTTGAATTAACATTAAGAGATTCAG 1260
Db 1201 CAGAGATCTTAGAGTACTGAGATGTTTCTTGAATTAACATTAAGAGATTCAG 1260
QY 1261 AAGTTAATGAGTGTTCAGAAAGTATGATGATGATGATGATGATGATGATGATGATG 1320

Db 1261 AAGTTAATGAGTGTTCAGAAAGTATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 GGGAGCTGAATCAAAATGCAAGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GGGAGCTGAATCAAAATGCAAGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 AATATCTGCTTCTGAGAGAAATAGACTTGTGAGAGTGTGAGAGTGTGAGAGTGT 1440
Db 1381 AATATCTGCTTCTGAGAGAAATAGACTTGTGAGAGTGTGAGAGTGTGAGAGTGT 1440
QY 1441 TATGTAAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 1441 TATGTAAAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
QY 1501 TTGGGAAAACCTATGGAAGAGGCAAGCTCCCAACCTTAAGCCATGTAAGTAAATC 1560
Db 1501 TTGGGAAAACCTATGGAAGAGGCAAGCTCCCAACCTTAAGCCATGTAAGTAAATC 1560
QY 1561 TAATTATGAGCATTTGTTTACTGAGCCACAGATTAATACAGAGGCTCCCTCAAAATA 1620
Db 1561 TAATTATGAGCATTTGTTTACTGAGCCACAGATTAATACAGAGGCTCCCTCAAAATA 1620
QY 1621 AATTAAAGGCTAAAGAGACCTACATCAGGCTTCTATCTGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAAGGCTAAAGAGACCTACATCAGGCTTCTATCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAAGATCTCTGAAATGATTAATAGGGAATCAACCAAGGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAAGATCTCTGAAATGATTAATAGGGAATCAACCAAGGAGC 1740
QY 1741 AGAATGCTCAATGATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1741 AGAATGCTCAATGATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 CTATTCAGATGAGAAAATCTTAACCCATGAAATCACTCGAAAAAGATCTGCTTGA 1860
Db 1801 CTATTCAGATGAGAAAATCTTAACCCATGAAATCACTCGAAAAAGATCTGCTTGA 1860
QY 1861 AAAAGAGCTGAACCTATTAAGCAGATTAAGCAATGAGAACTCGAAATTAATATTC 1920
Db 1861 AAAAGAGCTGAACCTATTAAGCAGATTAAGCAATGAGAACTCGAAATTAATATTC 1920
QY 1921 ACAATTCAAAACCTTAAGAAATAGGCTGAGAGGAGCTTCTACAGGCAATATTC 1980
Db 1921 ACAATTCAAAACCTTAAGAAATAGGCTGAGAGGAGCTTCTACAGGCAATATTC 1980
QY 1981 ATGCGCTTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
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QY 2041 TTGATATGTTTCTGACAGTGAAGATTAAGAAAAAGTAAACCAATGCCAGTCA 2100
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Db 2101 GGCACAGCAGAACTCAACATCATGGAAGTAAAGAACTTCAAGGCAAGAAAG 2160
QY 2161 GTAACAGCAGAACTCAACATCATGGAAGTAAAGAACTTCAAGGCAAGAAAG 2220
Db 2161 GTAACAGCAGAACTCAACATCATGGAAGTAAAGAACTTCAAGGCAAGAAAG 2220
QY 2221 AGTTAAACAAATGCACTGCTGTTTCTTACTGATGATGATGATGATGATGATGATG 2280
Db 2221 AGTTAAACAAATGCACTGCTGTTTCTTACTGATGATGATGATGATGATGATGATG 2280
QY 2281 TTGTCATCTGATGCTTCCAGAGAGAAAGAAAGATGATGATGATGATGATGATGATG 2340
Db 2281 TTGTCATCTGATGCTTCCAGAGAGAAAGAAAGATGATGATGATGATGATGATGATG 2340
QY 2341 CTAATTAATGCTGAGAAACCCCAAGATCTCATGTAAGTGAAGAGGTTTTCAGAACTG 2400

D	D	2341	CTAATATAGCTGAAGACCCCAAAAGATTCATGTTAACTGAGAAAGGGTTTGCAAACTG	2400
Q	Q	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTGACTGTGTACTGATTTATGGCACTGAG	2460
D	D	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTGACTGTGTACTGATTTATGGCACTGAG	2460
Q	Q	2461	AAAGTATCTGTAGAGAGTAGCAGTATTTCACTGTGACTGTGTACTGATTTATGGCACTGAG	2520
D	D	2461	AAAGTATCTGTAGAGAGTAGCAGTATTTCACTGTGACTGTGTACTGATTTATGGCACTGAG	2520
Q	Q	2521	GTGTGAGTCAAGTGTGAGCACTTTGAAAACCCCAAGGAGCTAATTCAGGTGTGTTCCAAG	2580
D	D	2521	GTGTGAGTCAAGTGTGAGCACTTTGAAAACCCCAAGGAGCTAATTCAGGTGTGTTCCAAG	2580
Q	Q	2581	ATTAATGAAATGACACAGAAAGGCTTTTAAGTATTCATTGGGACATGAAGTTAACCACAGTC	2640
D	D	2581	ATTAATGAAATGACACAGAAAGGCTTTTAAGTATTCATTGGGACATGAAGTTAACCACAGTC	2640
Q	Q	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTAACTGTAAGTCTCAGTATTTGCAAGATTCAT	2700
D	D	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTAACTGTAAGTCTCAGTATTTGCAAGATTCAT	2700
Q	Q	2701	TCGAAGTTTCAAGCCGCGACGTCATTTGCTGTGTTTCAATTCAGAAATGCAAGAGG	2760
D	D	2701	TCGAAGTTTCAAGCCGCGACGTCATTTGCTGTGTTTCAATTCAGAAATGCAAGAGG	2760
Q	Q	2761	AATGTGCAACATCTCTGCCCACTCGGGGCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
D	D	2761	AATGTGCAACATCTCTGCCCACTCGGGGCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Q	Q	2821	TTGAATGTGACAAAGAAAGAAATCAAGAAAGAAAGTGAAGTCTTAATATCAAGCTGTAC	2880
D	D	2821	TTGAATGTGACAAAGAAAGAAATCAAGAAAGAAAGTGAAGTCTTAATATCAAGCTGTAC	2880
Q	Q	2881	AAGACGTTAATATCACTGCAAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2940
D	D	2881	AAGACGTTAATATCACTGCAAGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2940
Q	Q	2941	ATGCCAAATGTAGTATCAAGAGAGGCTAGAGTTTGTCTATCATCTCAGTTCAGAGCA	3000
D	D	2941	ATGCCAAATGTAGTATCAAGAGAGGCTAGAGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Q	Q	3001	ACGAACTGGACCTCATTTACTCCAAATTAACATGACCTTTTACAAACCCTATCGTATAC	3060
D	D	3001	ACGAACTGGACCTCATTTACTCCAAATTAACATGACCTTTTACAAACCCTATCGTATAC	3060
Q	Q	3061	CACCACTTTTCCCATCAAGTCACTTTGTGTAACCTAATGTAAGAAATCTGTAGAG	3120
D	D	3061	CACCACTTTTCCCATCAAGTCACTTTGTGTAACCTAATGTAAGAAATCTGTAGAG	3120
Q	Q	3121	AAAACTTTGAGNAACATTCATGTCACTGAAAGAGAAATGGAAATGAGAACATTCOA	3180
D	D	3121	AAAACTTTGAGNAACATTCATGTCACTGAAAGAGAAATGGAAATGAGAACATTCOA	3180
Q	Q	3181	GTACGCTGAGCAACAATTAAGCCGTAATPAACATTAGAGAAATGTTTTAAAGAGCCAGCT	3240
D	D	3181	GTACGCTGAGCAACAATTAAGCCGTAATPAACATTAGAGAAATGTTTTAAAGAGCCAGCT	3240
Q	Q	3241	CAGCAATATTAATGAAGTAGTGTCCAGTACTAATGAAGTGGGCTCCAGATTATATGAA	3300
D	D	3241	CAGCAATATTAATGAAGTAGTGTCCAGTACTAATGAAGTGGGCTCCAGATTATATGAA	3300
Q	Q	3301	TAGGTTCCAGTGTGAAAACATTCAGCAACAACTAGGTAGAAACAGAGGGCCAAATTTGA	3360
D	D	3301	TAGGTTCCAGTGTGAAAACATTCAGCAACAACTAGGTAGAAACAGAGGGCCAAATTTGA	3360
Q	Q	3361	ATGCTATGCTTAATTAAGGAGTTTGGCACTTGAGGCTCTTAACCAAGTCTTCTGGA	3420
D	D	3361	ATGCTATGCTTAATTAAGGAGTTTGGCACTTGAGGCTCTTAACCAAGTCTTCTGGA	3420
Q	Q	3421	GTATTTGTAGCATCTGTAATTAAGAAAGCAAGATTTGAAGATGATTCAGCTGTA	3480
D	D	3421	GTATTTGTAGCATCTGTAATTAAGAAAGCAAGATTTGAAGATGATTCAGCTGTA	3480

QY	3481	ATACGATTTTCTCTCATATCTGATTTTCAGATACTTAGAACACGCTTAGTGAAGTAGTC	3540
Db	3481	ATACGATTTTCTCTCATATCTGATTTTCAGATACTTAGAACACGCTTAGTGAAGTAGTC	3540
QY	3541	ATGATCTCAGTTTGTCTGAGACACTGATGACCTGTAGATGATGTGAATAAAG	3600
Db	3541	ATGATCTCAGTTTGTCTGAGACACTGATGACCTGTAGATGATGTGAATAAAG	3600
QY	3601	AAGATATGATTTTGTCTGAAAAATGACATTAAGAAAGTTCTGCTTTTATGCAAAAGCG	3660
Db	3601	AAGATATGATTTTGTCTGAAAAATGACATTAAGAAAGTTCTGCTTTTATGCAAAAGCG	3660
QY	3661	TCCAGAGGAGAGGAGTTTGACAGAGTGCTTAGCCCTTACCCATACATTTGGCTCAGG	3720
Db	3661	TCCAGAGGAGAGAGGAGTTTGACAGAGTGCTTAGCCCTTACCCATACATTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCTTCAGAGAAGAACTTACTAGTAGATG	3780
Db	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCTTCAGAGAAGAACTTACTAGTAGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCAACACTTGTATTGGTAAGTAACAAATATACCTTTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAACACTTGTATTGGTAAGTAACAAATATACCTTTCAGT	3840
QY	3841	CTACTAGGCAATGACACGCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGATTTAT	3900
Db	3841	CTACTAGGCAATGACACGCGTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGATTTAT	3900
QY	3901	TATCATTTGAAGATATGCTTAATAATGACTGACGTAAACAGTATATTTGGCAAGGCATCTC	3960
Db	3901	TATCATTTGAAGATATGCTTAATAATGACTGACGTAAACAGTATATTTGGCAAGGCATCTC	3960
QY	3961	AGGAACATACACCTTAGTAGAGGAAAAAAATGTTGTAGTCTTTCTTCACAGTCA	4020
Db	3961	AGGAACATACACCTTAGTAGAGGAAAAAAATGTTGTAGTCTTTCTTCACAGTCA	4020
QY	4021	GTGAATTGGAAAGACTTGACTGCAAAATCAAAACCCAGAGTCCCTTCTGATTTGGTCTT	4080
Db	4021	GTGAATTGGAAAGACTTGACTGCAAAATCAAAACCCAGAGTCCCTTCTGATTTGGTCTT	4080
QY	4081	CCAAACAAATAGAGCATACGCTCTGAAAAAGCCAGGAGTTGCTGAGTGAACAAGAAATGG	4140
Db	4081	CCAAACAAATAGAGCATACGCTCTGAAAAAGCCAGGAGTTGCTGAGTGAACAAGAAATGG	4140
QY	4141	TTTCAGATGATGAAGAAAGGAAGCGGGCTTGAAGAATAATATCAAGAAGACCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAGCGGGCTTGAAGAATAATATCAAGAAGACCAAGCA	4200
QY	4201	TGATATTCAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCTCTTCTGAAG	4260
Db	4201	TGATATTCAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCTCTTCTGAAG	4260
QY	4261	ACTGTCACGGGCTTACCTCTCAGAGTACATTTTAACACATCAGCAGAGAGGATATACATGC	4320
Db	4261	ACTGTCACGGGCTTACCTCTCAGAGTACATTTTAACACATCAGCAGAGAGGATATACATGC	4320
QY	4321	AACATTAACCTGATAAAGCTCCAGAGAGAAATGCGTGAATCTAGAAAGCTGTATTGAACAGC	4380
Db	4321	AACATTAACCTGATAAAGCTCCAGAGAGAAATGCGTGAATCTAGAAAGCTGTATTGAACAGC	4380
QY	4381	ATGGAGCGACGCTTCTTAACAGCTAACCTTTCATCAATATGATGACTCTTTCGCCCTTGAGG	4440
Db	4381	ATGGAGCGACGCTTCTTAACAGCTAACCTTTCATCAATATGATGACTCTTTCGCCCTTGAGG	4440
QY	4441	ACCTGCGAAATCCAGAAACAAAGCAGATCCAGAAAAAGCAGATTAACTTCACAGAAAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAAACAAAGCAGATCCAGAAAAAGCAGATTAACTTCACAGAAAAAGTA	4500
QY	4501	GTGAATACCTTATAGCCAGAAATCCAGAAAGCCTTCTTCTGCTCAAGTTTGAGGTGCTG	4560
Db	4501	GTGAATACCTTATAGCCAGAAATCCAGAAAGCCTTCTTCTGCTCAAGTTTGAGGTGCTG	4560

QY 4561 CAGATAGTCTTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620
DB 4561 CAGATAGTCTTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620
QY 4621 GCCCATATTAAGATAGTGTGTAATGACAGTTCCTTGGAGTCTTCAAGATAGAA 4680
DB 4621 GCCCATATTAAGATAGTGTGTAATGACAGTTCCTTGGAGTCTTCAAGATAGAA 4680
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DB 5641 GTGTAGACTCTTACAGAGTCCAGAGAGCTGAGACCTGATATACCCAGATCCCCACA 5700
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DB 5701 GCCACTACTGA 5711
RESULT 8
AR033056 5711 bp DNA linear PAT 29-SEP-1999
LOCUS AR033056 Sequence 1 from patent US 5869245.
DEFINITION AR033056
ACCESSION AR033056
VERSION AR033056.1 GI:5948661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 5711)
TITLE Yeung, A.T.
JOURNAL Mismatch endonuclease and its use in identifying mutations in
FEATURES Targeted polynucleotide strands
Patent: US 5869245-A 1 09-FEB-1999;
location/Qualifiers
source 1..5711
BASE COUNT 1956 a 1099 c 1274 g 1382 t
ORIGIN
Query Match 99.8%; Score 5699.8; DB 6; Length 5711;
Best Local Similarity: 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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DB 1 AGCTGCTAGACTTCTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAATATCTGGCC 60
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DB 61 CCGGCGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAGTTCATTGGAACGAAAGAA 120
QY 121 TGAATTTATCTGCTCTTCCGCTTGAAGAAATGTCATTAATGCTATGACGAAA 180
DB 121 TGAATTTATCTGCTCTTCCGCTTGAAGAAATGTCATTAATGCTATGACGAAA 180
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DB 181 TCTTAGAGTGTCCCATCTGTGTGAGTTGATCAAGAACCTGTCTCCACAAAGTGTGAC 240
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QY 301 GTCTTTATATGATGATGATATTAACCAAGAGGCTTCAAGAAATGACGATTTAGTC 360
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DB 541 AACCCGAAATCTCTTCTTGCAGAAACCAAGTCTAGAGTCCAACTCTTAACTTTGAA 600

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QY 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGAGAA 1020
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QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATGAAGCAAACTGCCATGCT 1200
| | | | |
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATGAAGCAAACTGCCATGCT 1200
QY 1201 CAGAGAACTCTGAGATCTGAAGATGTTCTTGATTAACCTAAATAGCAGATTCAGA 1260
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complete cds.
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VERSION 1
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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JOURNAL Science 266 (5182), 66-71 (1994)
MEDLINE 95025896
PUBMED 7545954
REFERENCE 2 (bases 1 to 5711)
AUTHORS Skolnick,M.H.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and
the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City,
UT 84108, USA
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QY	541	AAACCGAAATCTCTTCCTTGCAGGAAACAGTCTCAGTCCAACTCTTAACTTTGGAA	600
Db	541	AAACCGAAATCTCTTCCTTGCAGGAAACAGTCTCAGTCCAACTCTTAACTTTGGAA	600
QY	601	CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTG	660
Db	601	CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATTG	660
QY	661	AATTGGGATCGATTCTTCTGAGATCCGTTATTAAGGCAACTTATGCAAGTGGGAG	720
Db	661	AATTGGGATCGATTCTTCTGAGATCCGTTATTAAGGCAACTTATGCAAGTGGGAG	720
QY	721	ATCAAGAAATTTTCAAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTTGGATTCTG	780
Db	721	ATCAAGAAATTTTCAAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTTGGATTCTG	780
QY	781	CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAAACAATATCTGAACATCATCAAC	840
Db	781	CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAAACAATATCTGAACATCATCAAC	840
QY	841	CCAGTAATAAGATTTTGAACAACAACCTGAGAGCGTGAAGGATCCAAAAAGT	900
Db	841	CCAGTAATAAGATTTTGAACAACAACAACCTGAGAGCGTGAAGGATCCAAAAAGT	900
QY	901	ATCAGGGTACTTCTGTTCAAACTTGCATGTGAGACCATGTGGCAAAATCTCATGCA	960
Db	901	ATCAGGGTACTTCTGTTCAAACTTGCATGTGAGACCATGTGGCAAAATCTCATGCA	960
QY	961	GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGAATGTGAAA	1020
Db	961	GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGAATGTGAAA	1020
QY	1021	AGGCTGAATTTGTAAATTAAGCAAAACAGCTGGCTTACGAAGAGCCAAATATACGAT	1080
Db	1021	AGGCTGAATTTGTAAATTAAGCAAAACAGCTGGCTTACGAAGAGCCAAATATACGAT	1080
QY	1081	GGGCTGGAAGTAAGAAACATGTATATAGTAGGCGAATCCAGACACAGAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGAAACATGTATATAGTATAGGCGAATCCAGACACAGAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATATAGCAGAACTGCTATGCT	1200


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Db 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAGATGAAATGAAGCAAGAACTGCCATGCT 1200
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Qy 2041 TTGATAGTGTCTTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCAAGTCA 2100
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[illegible]

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Db	4501	GTGAATACCCATATAAGCAGAAATCCAGAAAGCCCTTTCTGCTGACAAAGTTGAGGTGCTG	4560
QY	4561	CAGATAGTTCTTACCGATTAATAAAGAACGAGAGTGGAAAAGGTCAATCCCTTTCTAAAT	4620
Db	4561	CAGATAGTTCTTACCGATTAATAAAGAACGAGAGTGGAAAAGGTCAATCCCTTTCTAAAT	4620
QY	4621	GCCCATCTATTAGATGATAGTGGGTACATGCACAGTTGCTCTGGGAGTCTTACAGATTAGAA	4680
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QY	4661	ACTACCCATCTCCAGAGAGCTCAATTAAAGTTGTGATGTGAGAGAGCAACAGCTGGAG	4740
Db	4661	ACTACCCATCTCCAGAGAGCTCAATTAAAGTTGTGATGTGAGAGAGCAACAGCTGGAG	4740
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Db	4981	ATACTGCTGGGTATTAATGCAATGSAAGAAAGTGTGACGAGGAGAACCCAGAAATTGACAG	5040
QY	5041	CTTCAACGAAAGGGTCAACAAAGAAATGTCATGATGTGTCTGGGCTGACCCCAAG	5100
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DEFINITION Sequence 1 from patent US 5891857.
ACCESSION AR070223
VERSION AR070223.1 GI:7221111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holte,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,
Jettion,T.L., Robinson-Benion,C.L. and Thompson,M.E.
TITLE Characterized BRCA1 and BRCA2 proteins and screening and
JOURNAL Patent: US 5891857-A 1 06-APR-1999;
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Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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AUTHORS Holt, J.T., Jensen, R.A., King, M.-C., Page, D.L., Szabo, C.I.,
 Jettison, T.L., Robinson-Benion, C.L. and Thompson, M.E.
 TITLE Characterized BRCA1 and BRCA2 proteins and screening and
 therapeutic methods based on characterized BRCA1 and BRCA2 proteins
 JOURNAL Patent: US 6149303-A 1 21-NOV-2000;
 FEATURES Location/Qualifiers
 source 1.5712
 /organism="unknown"

BASE COUNT 1956 a 1099 c 1274 g 1383 t
 ORIGIN

Query Match 99.8%; Score 5699.8; DB 6; Length 5712;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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ACCESSION ARI25601
VERSION ARI25601.1 GI:14111663
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Db 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAACCTTCAAAAGAGCTGTCTTCAATTTG 660
Qy 661 AATTGGGATCTGATCTCTGAGATACCGTTAATAGGCACTTATGCACTGTGGGAG 720
Db 661 AATTGGGATCTGATCTCTGAGATACCGTTAATAGGCACTTATGCACTGTGGGAG 720
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Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGAACAAATCTGAAACATCATCAAC 840
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Db 841 CCAGTAATTAATGATTTGAAACCACTGAGAAAGCTGAGAGGCACTCCAGAAAGT 900
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DB 2521 GGTGAGTCAAGTGTGAGCATTTGAAAACCCCAAGGACCTAATCTAGTGTGTTCCAAAG 2580
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QY 4561 CAGATAGTTCTACAGTAAAAATAAGAACAGAGAGTGAAGAGTCAATCCCTTAAAT 4620

Db	4561	CAGATAGTCTTACCACTAATAAATAAGAACCAAGAGTGGAAAGTCAATCCCTTTAAAT	4620
Oy	4621	GGCCATCATTTAGATGATAGGTGGTACATGACAGTTGCTCTGGAGTCTTCAGAAATAGA	4680
Db	4621	GGCCATCATTTAGATGATAGGTGGTACATGACAGTTGCTCTGGAGTCTTCAGAAATAGA	4680
Oy	4681	ACTACCCATCTCAAGGGAGGCTCATTTAAGGTGGTTGATGTGGAGAGCAACGCTGGAA	4740
Db	4681	ACTACCCATCTCAAGGGAGGCTCATTTAAGGTGGTTGATGTGGAGAGCAACGCTGGAA	4740
Oy	4741	AGTCTGGGCCACACGATTTTGACGGAAACATCTTACTTTCGAAGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTTGACGGAAACATCTTACTTTCGAAGCAAGATCTAGAGGAA	4800
Oy	4801	CCCCCTTACCTGGAAATCTGGAAATCACGCTCTTCTGTGATGACCTGTAATCTGATCCCTTG	4860
Db	4801	CCCCCTTACCTGGAAATCTGGAAATCACGCTCTTCTGTGATGACCTGTAATCTGATCCCTTG	4860
Oy	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGGCAACATACATCTTCAACCTTCGATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGGCAACATACATCTTCAACCTTCGATTTGA	4920
Oy	4921	AAGTTTCCCCAATTGAAAGTTTGACGAATCTGCCAGGTCACGCTGCTCTATACTG	4980
Db	4921	AAGTTTCCCCAATTGAAAGTTTGACGAATCTGCCAGGTCACGCTGCTCTATACTG	4980
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Db	4981	ATACTGCTGGGTATATGCAATGAGAAAGTGTGAGAGAGGAGAAAGCAGAAATTGACAG	5040
Oy	5041	CTTCAACAGAAAGGCTCAACAAAGATGTCCATGCTGGTGTCTGGCTGACCCCAAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGATGTCCATGCTGGTGTCTGGCTGACCCCAAG	5100
Oy	5101	AATTATGCTGCTGATCAAGTTTGCAGAAAACACCAATCACTTAACTAATCTAATTA	5160
Db	5101	AATTATGCTGCTGATCAAGTTTGCAGAAAACACCAATCACTTAACTAATCTAATTA	5160
Oy	5161	CTGAAGAGACTACCTAGTGTGTTATGAAAAACAGATGCTGAGTTTGTGTGAACGGAC	5220
Db	5161	CTGAAGAGACTACCTAGTGTGTTATGAAAAACAGATGCTGAGTTTGTGTGAACGGAC	5220
Oy	5221	TGAATATTTTCTAGGAATGTGGGGAGGAAAAATGGGTAGTATTTCTGGGGTGAACC	5280
Db	5221	TGAATATTTTCTAGGAATGTGGGGAGGAAAAATGGGTAGTATTTCTGGGGTGAACC	5280
Oy	5281	AGCTATTAAAGAAAGAAATAGCTGATGAGCATGATTTTGAAATGCAGAGAGATGTGG	5340
Db	5281	AGCTATTAAAGAAAGAAATAGCTGATGAGCATGATTTTGAAATGCAGAGAGATGTGG	5340
Oy	5341	TCAATGGAAGAAACCAACAGGTCCAAACCGACGAAGAAATCCAGAGCAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACAGGTCCAAACCGACGAAGAAATCCAGAGCAGAAAGATCT	5400
Oy	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCCCACAGATCACTGG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCCCACAGATCACTGG	5460
Oy	5461	AATGATGATCAGCTGTGTGCTTCTGTGTGAAGAGCTTTCATCATTTACCTTGG	5520
Db	5461	AATGATGATCAGCTGTGTGCTTCTGTGTGAAGAGCTTTCATCATTTACCTTGG	5520
Oy	5521	GCACAGGTGTCCACCAATTGTGTGTGACACAGATGCTCGGACAGAGGACAAATGGCT	5580
Db	5521	GCACAGGTGTCCACCAATTGTGTGTGACACAGATGCTCGGACAGAGGACAAATGGCT	5580
Oy	5581	TTCATGCAATTGGGAGATGTGTGAGGCACTGTGGTGAACCCGAGATGTGGTGTGACA	5640
Db	5581	TTCATGCAATTGGGAGATGTGTGAGGCACTGTGGTGAACCCGAGATGTGGTGTGACA	5640
Oy	5641	GTTGAGCACTTACCAAGTCCAGAGCTGGACAACCTAATCTGATACCCAGATCCCCACA	5700

Db	5641	GTGTAGCACTGTACACGAGCCAGAGAGCTGACACCTGATATACCCAGATCCCCCACA	5700
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Db	5701	GGCACTACTGA 5711	
RESULT 13			
AR184044			
LOCUS	AR184044	5712 bp	DNA
DEFINITION	Sequence 47 from patent US 6342483.		linear
ACCESSION	AR184044		
VERSION	AR184044.1	GI:20228013	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 5712)		
TITLE	Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S., Robinson-Bentley,C.L. and Thompson,M.E.		
JOURNAL	Method for detection and treatment of breast cancer		
FEATURES	Patent: US 6342483-A 47 29-JUN-2002;		
source	location/qualifiers		
	1..5712		
BASE COUNT	1956 a 1099 c 1274 g 1383 t		
ORIGIN			
Query Match	99.8%; Score 5699.8; DB 6; Length 5712;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 5704; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		
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Db	1	AGCTGCTGAGACTTCTCTGGAACCCCGACACAGGCTGTGGGTTTCTCAGATPACTGGGCC	60
Qy	61	CCTGGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTAAAGTCAATGGAA CAGAAAGAA	120
Db	61	CCTGGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTAAAGTCAATGGAA CAGAAAGAA	120
Qy	121	TGATTTATCTGCTCTTTCGCGTTGAGAGATCAAAAATGTCATTAAATGCTATG CAGAAA	180
Db	121	TGATTTATCTGCTCTTTCGCGTTGAGAGATCAAAAATGTCATTAAATGCTATG CAGAAA	180
Qy	181	TCTTAGAGATGCCCATCTGTCTGAGAGTTCAGAGAACCTGTCTCCACAAAGTGTACC	240
Db	181	TCTTAGAGATGCCCATCTGTCTGAGAGTTCAGAGAACCTGTCTCCACAAAGTGTACC	240
Qy	241	ACATATTTTGGAAATTTTGGCATGCTGAAACCTTCCACAGAGAAAGAGGCGCTT CACAGT	300
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Qy	301	GTCCTTTATGTAGATGATATAACCAAAAGAGCCTTACAGAAAGTACGAGATTAGTC	360
Db	301	GTCCTTTATGTAGATGATATAACCAAAAGAGCCTTACAGAAAGTACGAGATTAGTC	360
Qy	361	AACCTGTTGAAGAGCTATGGAATTCATTTTGCTTTTCAGCTTGACACAGGTTGGAGT	420
Db	361	AACCTGTTGAAGAGCTATGGAATTCATTTTGCTTTTCAGCTTGACACAGGTTGGAGT	420
Qy	421	ATGCAAAACAGCTATATTTTGCACAAAAGGAAATTAATCTCTCTGAAATCTTAAGAATG	480
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Qy	481	AAAGTTTCTATATCAACAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTTACAGAGTG	540
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Qy	541	AAACCGGAAATATCTTCTCTGAGAGAAACAGTCTCAAGTGTCAACTCTTAACTTTGGAA	600
Db	541	AAACCGGAAATATCTTCTCTGAGAGAAACAGTCTCAAGTGTCAACTCTTAACTTTGGAA	600
Qy	601	CTGTGAGAACTCTGAGAGCAAGAGCGAGATACAACCTCAAAAGACGTCTGTCTTACATTG	660

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Db 601 CTGTGGAACCTCGAGAGACAAAGCAGGATACAACTCAAAAGAGTCTGTCTACATG 660
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Qy 1561 TAAATTTAGAGATTTGTTTACTGAGCCACAGATATTAACAAGGCTCCCTCCACAAAAT 1620
Db 1561 TAAATTTAGAGATTTGTTTACTGAGCCACAGATATTAACAAGGCTCCCTCCACAAAAT 1620
Qy 1621 AATTAAGGCTAAAGAGACCTACATCAGGCTTATCCTGAGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGGCTAAAGAGACCTACATCAGGCTTATCCTGAGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGCGATTTCAAAAGACTCTGAAATGATTAATCAGGAACTAAACAAACGAGAC 1740
Db 1681 CAGATTTGCGATTTCAAAAGACTCTGAAATGATTAATCAGGAACTAAACAAACGAGAC 1740

Db 1681 CAGATTTGCGAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTAAACAAACGAGAC 1740
Qy 1741 AGAATGCTCAAGTGAATATTTACTAATAGTGGTCAATGAGATTAATAACAAAGGATTT 1800
Db 1741 AGAATGCTCAAGTGAATATTTACTAATAGTGGTCAATGAGATTAATAACAAAGGATTT 1800
Qy 1801 CTATTCAGAAAGGAAATCTTAAACCAATGAAATCACTCGAAAAGAAATCTGCTTTCA 1860
Db 1801 CTATTCAGAAAGGAAATCTTAAACCAATGAAATCACTCGAAAAGAAATCTGCTTTCA 1860
Qy 1861 AAACGAAAGCTGACCTATTAACAGAGATTAAGCAATATGGAATCTCGAATTAATATTC 1920
Db 1861 AAACGAAAGCTGACCTATTAACAGAGATTAAGCAATATGGAATCTCGAATTAATATTC 1920
Qy 1921 ACAATTTCAAAACCTTAAAGAAATAGGCTGAGAGAAAGTCTTACAGGCAATATTC 1980
Db 1921 ACAATTTCAAAACCTTAAAGAAATAGGCTGAGAGAAAGTCTTACAGGCAATATTC 1980
Qy 1981 ATGCGCTTGAACTAGTACATGAGAAATCTAAGCCCACTTAATTTGACTGAATTCGAA 2040
Db 1981 ATGCGCTTGAACTAGTACATGAGAAATCTAAGCCCACTTAATTTGACTGAATTCGAA 2040
Qy 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCCAGTCA 2100
Db 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCCAGTCA 2100
Qy 2101 GGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTGCAACCTGAGCCAGAAAGA 2160
Db 2101 GGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTGCAACCTGAGCCAGAAAGA 2160
Qy 2161 GTAAAGCCAAATGAACAGACAGAAAGATTAAGAAAGATGATCTTTCCAGAGCTGA 2220
Db 2161 GTAAAGCCAAATGAACAGACAGAAAGATTAAGAAAGATGATCTTTCCAGAGCTGA 2220
Qy 2221 AGTTAAACAATGCACTGTTCTTTTACTAAGTGTTCAAATACAGTGAATTTAAAGAT 2280
Db 2221 AGTTAAACAATGCACTGTTCTTTTACTAAGTGTTCAAATACAGTGAATTTAAAGAT 2280
Qy 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAGAACTAAGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAGAACTAAGAAACAGTTAAAGTGT 2340
Qy 2341 CTAATATGCTGAAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAAACTG 2400
Db 2341 CTAATATGCTGAAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAAACTG 2400
Qy 2401 AAAGATCTGTAGAGATGACAGTATTTCACTGTGATCTGATTAAGCACTCAGG 2460
Db 2401 AAAGATCTGTAGAGATGACAGTATTTCACTGTGATCTGATTAAGCACTCAGG 2460
Qy 2461 AAAGATCTGTTACTGGAAGTATGACCTTAAGGAGGCAAAACAGAAACCAATTAAT 2520
Db 2461 AAAGATCTGTTACTGGAAGTATGACCTTAAGGAGGCAAAACAGAAACCAATTAAT 2520
Qy 2521 GTGTAGTCAAGTGTGACAGATTTGAAAACCCCAAGGACTAATTCATGTTTCCAAAG 2580
Db 2521 GTGTAGTCAAGTGTGACAGATTTGAAAACCCCAAGGACTAATTCATGTTTCCAAAG 2580
Qy 2581 ATTAATGAATGACACAGAAAGCTTTAAATGATCAATGGACATGAAGTTAACACAGTC 2640
Db 2581 ATTAATGAATGACACAGAAAGCTTTAAATGATCAATGGACATGAAGTTAACACAGTC 2640
Qy 2641 GGGAAACAAAGCTAATAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
Db 2641 GGGAAACAAAGCTAATAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
Qy 2701 TCAAGTTTCAAGGCGCAGTATTTGCTGTTTCAATTCAGAGAAATGAGAGAGG 2760
Db 2701 TCAAGTTTCAAGGCGCAGTATTTGCTGTTTCAATTCAGAGAAATGAGAGAGG 2760
Qy 2761 AATGTGCAACATTTCTGCGCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGCGCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820

QY	1021	AGCGTGAATTCGTGTAATTAAGCAACAGCTGGCTTGACAAAGGACCAATTAACAGAT	1080
Db	1021	AGCGTGAATTCGTGTAATTAAGCAACAGCTGGCTTGACAAAGGACCAATTAACAGAT	1080
QY	1081	GGCGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACCTCCGACGACACAAAAAAAGGTAG	1140
Db	1081	GGCGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACCTCCGACGACACAAAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAATAGCAGAAACTGCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAATAGCAGAAACTGCCATGCT	1200
QY	1201	CAGAGAAATCTTAGAATACTGAAGTGTTCCTTGGATTAACCTAATATGCAGCATTTGCA	1260
Db	1201	CAGAGAAATCTTAGAATACTGAAGTGTTCCTTGGATTAACCTAATATGCAGCATTTGCA	1260
QY	1261	AAGTAAATGAGAGGTTCCTCAGAAATGATGAACTGTAGGTTCTGTAGATCACTAGTATG	1320
Db	1261	AAGTAAATGAGAGGTTCCTCAGAAATGATGAACTGTAGGTTCTGTAGATCACTAGTATG	1320
QY	1321	GGGAGCTGGAATCAATGCGCAAGTAGCTGATGTTTGGACGTTTCTAATAGAGGTAGATG	1380
Db	1321	GGGAGCTGGAATCAATGCGCAAGTAGCTGATGTTTGGACGTTTCTAATAGAGGTAGATG	1380
QY	1381	AATATATTCGTGTTCTTCAGAGAAATATAGACTTCTGGCCAGTGATCTCATAGGCTTTAA	1440
Db	1381	AATATATTCGTGTTCTTCAGAGAAATATAGACTTCTGGCCAGTGATCTCATAGGCTTTAA	1440
QY	1441	TATGTAAAGATGAAAGAGTTCACTCCCAATCGTAGAGATTAATTTGAAGACAAATAT	1500
Db	1441	TATGTAAAGATGAAAGAGTTCACTCCCAATCGTAGAGATTAATTTGAAGACAAATAT	1500
QY	1501	TTGGGAAAACTTATCGGAAGAGGAGCGCTCCCACTTAAGCCATGTAACGTGAAATC	1560
Db	1501	TTGGGAAAACTTATCGGAAGAGGAGCGCTCCCACTTAAGCCATGTAACGTGAAATC	1560
QY	1561	TAATTAATAGAGCACTTTGTTACTGACCAAGATTAATCAAGAGCGTCCCTCACAAATA	1620
Db	1561	TAATTAATAGAGCACTTTGTTACTGACCAAGATTAATCAAGAGCGTCCCTCACAAATA	1620
QY	1621	AATTAACCGTAAAGAGAGCCTACATCAGGCTTCATCCGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAACCGTAAAGAGAGCCTACATCAGGCTTCATCCGAGGATTTTATCAAGAAAG	1680
QY	1681	CAGATTTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAACCTAACCAACGAGC	1740
Db	1681	CAGATTTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAACCTAACCAACGAGC	1740
QY	1741	AGAAATGCTCAAGTGAATTAATTAATTAATGAGGTCAATGAGATTAACCAAAAGGTGAT	1800
Db	1741	AGAAATGCTCAAGTGAATTAATTAATTAATGAGGTCAATGAGATTAACCAAAAGGTGAT	1800
QY	1801	CTATTACAGATGAGAAAAAATCCTTACCAATAGATCACTCGAAATAAATCTGCTTCA	1860
Db	1801	CTATTACAGATGAGAAAAAATCCTTACCAATAGATCACTCGAAATAAATCTGCTTCA	1860
QY	1861	AAACGAAAGCTGAACTTAATAGCAGCAGATTAAGCAATATGGAATCTCAATTAATAATCC	1920
Db	1861	AAACGAAAGCTGAACTTAATAGCAGCAGATTAAGCAATATGGAATCTCAATTAATAATCC	1920
QY	1921	ACAAATTTCAAAAGCACTTAATAAGATTAAGGCTGAGGAGGAGTCTTCAACAGGCATATC	1980
Db	1921	ACAAATTTCAAAAGCACTTAATAAGATTAAGGCTGAGGAGGAGTCTTCAACAGGCATATC	1980
QY	1981	ATGCGCTTGAATCTAGTACTAGTAAATCTTAAGCCCACTTAATTTGTACTGAATTTGCATA	2040
Db	1981	ATGCGCTTGAATCTAGTACTAGTAAATCTTAAGCCCACTTAATTTGTACTGAATTTGCATA	2040
QY	2041	TTGATAGTTGTTCTTACAGTGAAGAGATTAAGAAAAAAAGTACAAACAAATGCGACATCA	2100
Db	2041	TTGATAGTTGTTCTTACAGTGAAGAGATTAAGAAAAAAAGTACAAACAAATGCGACATCA	2100
QY	2101	GGCACAGCAGAAACCTCAACACTCATGGAAGGTAAAGAACTTGCACTGAGCCCAAGAGA	2160

Db	2101	GGCAGAGAGAAAGCTTACACTCAGTAGAAGGTAAAGAACTCGCAACTGGAACCAAGAA	2160
Qy	2161	GTAAACAAGCCAAATGATGAGACAAGATAAAGATGACAGTATATCTTTCCAGAGCTGA	2220
Db	2161	GTAAACAAGCCAAATGATGAGACAAGATAAAGATGACAGTATATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAATGACACTCTGTTCTTTTACTAAGTGTCAATATGCAATGAACTTAAAGAT	2280
Db	2221	AGTTAAACAATGACACTCTGTTCTTTTACTAAGTGTCAATATGCAATGAACTTAAAGAT	2280
Qy	2281	TTGTCAATCCTAGACCTTCCAAAGAGAAGAAAGAAAGAAACCTGAAACGTTAAAGGT	2340
Db	2281	TTGTCAATCCTAGACCTTCCAAAGAGAAGAAAGAAAGAAACCTGAAACGTTAAAGGT	2340
Qy	2341	CTAATAATAGCTGAAAGACCCCAAGATCTCATGTGTAAGTGAAGAGGTTTGGCAACTG	2400
Db	2341	CTAATAATAGCTGAAAGACCCCAAGATCTCATGTGTAAGTGAAGAGGTTTGGCAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGACAGTATTTCACTGTGACTGTACTGATTTATGGCACTAG	2460
Db	2401	AAAGATCTGTAGAGAGTAGACAGTATTTCACTGTGACTGTACTGATTTATGGCACTAG	2460
Qy	2461	AAAGATCTCGTTACTGTGAAGTGAACCTGAAAGAGGCAAAAACGAACCAATTAAT	2520
Db	2461	AAAGATCTCGTTACTGTGAAGTGAACCTGAAAGAGGCAAAAACGAACCAATTAAT	2520
Qy	2521	GTGTAGTCAGTGTGCAAGCTTTTGGAAACCCCAAGAGGCAATTCATGTGTTGCCAAG	2580
Db	2521	GTGTAGTCAGTGTGCAAGCTTTTGGAAACCCCAAGAGGCAATTCATGTGTTGCCAAG	2580
Qy	2581	ATATATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGAGCATGAAGTTAACCAAGTC	2640
Db	2581	ATATATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGAGCATGAAGTTAACCAAGTC	2640
Qy	2641	GGGAAACAAAGCATAGAAATGGAAGAAATGAACCTGATGCTCAGTATTTGGAGAATCAT	2700
Db	2641	GGGAAACAAAGCATAGAAATGGAAGAAATGAACCTGATGCTCAGTATTTGGAGAATCAT	2700
Qy	2701	TCAAGGTTTCAAAGGCGCAGTCATTTGGTCTGTTTCAATATCCAGAAATGCAGAAAGG	2760
Db	2701	TCAAGGTTTCAAAGGCGCAGTCATTTGGTCTGTTTCAATATCCAGAAATGCAGAAAGG	2760
Qy	2761	AATGTGCAACATCTCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAACATCTCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGACAGCTTTCTGTGGTTGGTCAGAAAGATTAAGCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGACAGCTTTCTGTGGTTGGTCAGAAAGATTAAGCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Db	2941	ATGCCAAATGTAGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Qy	3001	ACGAAACTGGAAGCTATTAATCAAAATGAAGATGAGCTTTTACAAACCATATCGTATAC	3060
Db	3001	ACGAAACTGGAAGCTATTAATCAAAATGAAGATGAGCTTTTACAAACCATATCGTATAC	3060
Qy	3061	CACCACTTTTCCATCAAGTCACTTGTGTAATACTAATGTAAAGAAATCTGCTAAGG	3120
Db	3061	CACCACTTTTCCATCAAGTCACTTGTGTAATACTAATGTAAAGAAATCTGCTAAGG	3120
Qy	3121	AAAACTTTGAGAAACATTCAATGTCACTGAAGAAATGGGAAATGAGAAACATTGCCA	3180
Db	3121	AAAACTTTGAGAAACATTCAATGTCACTGAAGAAATGGGAAATGAGAAACATTGCCA	3180
Qy	3181	GTACAGTGAACAATTAGCCGTATATACATTAGAGAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAACAATTAGCCGTATATACATTAGAGAAATGTTTTTAAAGAGCCAGCT	3240

3181 GTACAGTACGACAAATTAGCCGTAATTAACATTAGAGAAAATGTTTTAAAGAACCGAGCT 3240
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3242 CAAGCAATATTAAATGAAGTAGTTCAGTACTAATGAAGTGGCTCAGATTAATGAAG 3300
3301 TAGGTTCCAGTGAATGAAGCAATTCAGAGCAAGTATGAGAAACAGAGGCGCAAAATGA 3360
3302 TAGGTTCCAGTGAATGAAGCAATTCAGAGCAAGTATGAGAAACAGAGGCGCAAAATGA 3360
3361 ATGCTATGCTTAATTAATGAGGAGTTTTCAGACCTGAGCTCTAATCAAAAGCTTCTGGA 3420
3362 ATGCTATGCTTAATTAATGAGGAGTTTTCAGACCTGAGCTCTAATCAAAAGCTTCTGGA 3420
3421 GTATTTGTAAGCATCTCTGAAATTAAGAAAGCAAGATATGAGAAAGTAGTTCAAGCTGTA 3480
3422 GTATTTGTAAGCATCTCTGAAATTAAGAAAGCAAGATATGAGAAAGTAGTTCAAGCTGTA 3480
3481 ATACAGATTTCTCTCAATATCTGATTTCAATTAAGTAAAGCTATGAGAAAGTAGTTC 3540
3482 ATACAGATTTCTCTCAATATCTGATTTCAATTAAGTAAAGCTATGAGAAAGTAGTTC 3540
3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGTATGTTGAATTAAG 3600
3542 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGTATGTTGAATTAAG 3600
3601 AAGATCTAGTTTGTCTGAAATTAAGCAATTAAGAAAGTCTGCTGTTTAAAGAAAGG 3660
3602 AAGATCTAGTTTGTCTGAAATTAAGCAATTAAGAAAGTCTGCTGTTTAAAGAAAGG 3660
3661 TCCAGAGAGAGAGCTTACAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAG 3720
3662 TCCAGAGAGAGAGCTTACAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAG 3720
3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGAGAGT 3780
3722 GTTACCGAAGAGAGGCGCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGAGAGT 3780
3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTTAAAGTAATTAATTAATTAATTAATTA 3840
3782 AAGAGCTTCCCTGCTTCCAACTTGTATTTGTTAAAGTAATTAATTAATTAATTAATTA 3840
3841 CTACTAGGCAATAGCACGTTGCTACCAAGTCTGTCTAAGAACACAGAGAGAAATTA 3900
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3961 AAGAACTACCTTATGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
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4142 TTTCAATGATGAAGAAAG 4200
4201 TGGATTTCAAACTTGAAG 4260
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4321 AACATTAACCTGATTAAGAGCTCCAGAGAGAAATGCTGAATTAAGAGAGAGAGAGAGAG 4380
4322 AACATTAACCTGATTAAGAGCTCCAGAGAGAAATGCTGAATTAAGAGAGAGAGAGAGAG 4380
4381 ATGGAG 4440
4382 ATGGAG 4440
4441 ACCGAG 4500
4442 ACCGAG 4500
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4561 CAGATTAATCTCAAG 4620
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4621 GCCCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
4622 GCCCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680
4681 ACTACCATCTCAAG 4740
4682 ACTACCATCTCAAG 4740
4741 AGCTGGGCGCACAGATTTGAGAGAAACATCTTACCTTCCAGAGAGAGAGAGAGAGAGAG 4800
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4801 CCCCTTACCTGAG 4860
4802 CCCCTTACCTGAG 4860
4861 AAG 4920
4862 AAG 4920
4921 AAGTTCCCAATTTGAAG 4980
4922 AAGTTCCCAATTTGAAG 4980
4981 AATCTGCTGGGTATTAATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040
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5041 CTTCAACAGAAAG 5100
5042 CTTCAACAGAAAG 5100
5101 AATTTATGCTGTGATGAAG 5160
5102 AATTTATGCTGTGATGAAG 5160
5161 CTGAAG 5220
5162 CTGAAG 5220
5221 TGAATTAATTTTATGAAG 5280
5222 TGAATTAATTTTATGAAG 5280
5281 AGCTTAATTAAG 5340
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5341 TCAATGAAG 5400
5342 TCAATGAAG 5400

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 DB 1441 TATGTAAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATAATATTGGAAGCAAAATAT 1500
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 DB 1561 TAAATATAGAGCATTGTGTACTGAGCCACAGATTAATAGAGAGTCCCTCCACAAAAT 1620
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 DB 1621 AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680
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 QY 1741 AAGATGCTCAAGTGAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1800
 DB 1741 AAGATGCTCAAGTGAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1800
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 DB 1921 ACAATTCAGAAACCTTAAGAAATAGAGTGAAGAGAGAGTCTTCAACGAGCATATTC 1980
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 DB 3181 GTACAGTGAACCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3240
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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 15338361 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	1	US-08-798-691-3 Sequence 3, Appl1
2	5711	100.0	5711	3	US-08-825-487A-3 Sequence 3, Appl1
3	5711	100.0	5711	3	US-09-074-476-5 Sequence 5, Appl1
4	5709.4	100.0	5711	2	US-08-658-322-1 Sequence 1, Appl1
5	5709.4	100.0	5712	2	US-08-603-753D-1 Sequence 1, Appl1
6	5709.4	100.0	5712	3	US-09-099-753-1 Sequence 1, Appl1
7	5709.4	100.0	5712	4	US-08-986-106-1 Sequence 1, Appl1
8	5709.4	100.0	5712	4	US-09-007-678B-47 Sequence 47, Appl1
9	5709.4	100.0	5914	1	US-08-480-784-1 Sequence 1, Appl1
10	5709.4	100.0	5914	1	US-08-483-553-1 Sequence 1, Appl1
11	5709.4	100.0	5914	1	US-08-487-002-1 Sequence 1, Appl1
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15	5709.4	100.0	5914	5	PCT-US95-10202-1 Sequence 1, Appl1
16	5709.4	100.0	5914	5	PCT-US95-10203-1 Sequence 1, Appl1
17	5709.4	100.0	5914	5	PCT-US95-10220-1 Sequence 1, Appl1
18	5707.8	99.9	5711	1	US-08-425-061-4 Sequence 4, Appl1
19	5707.8	99.9	5711	1	US-08-425-061-10 Sequence 10, Appl1
20	5707.8	99.9	5711	1	US-08-825-886-4 Sequence 4, Appl1
21	5707.8	99.9	5711	1	US-08-825-886-10 Sequence 10, Appl1
22	5703	99.9	5711	3	US-08-798-691-5 Sequence 5, Appl1
23	5703	99.9	5711	3	US-08-825-061-7 Sequence 7, Appl1
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45	5629.2	98.6	5770	1	US-08-425-061-5 Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-798-691-3
; Sequence 3, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antoinette C.
; APPLICANT: Alvaras, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCOMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos
REGISTRATION NUMBER: 32,692
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17

MAP POSITION: 17q21
US-08-798-691-3

Query Match 100.0%; Score 5711; DB 1; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2701 TCAGAGTTTCAAGGCGCCAGTCTTGTCTGTCTTCAATCCAGAAATGCGAAGAGG 2760
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Db 2701 TCAGAGTTTCAAGGCGCCAGTCTTGTCTGTCTTCAATCCAGAAATGCGAAGAGG 2760
QY 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAACAAATGCCAAAGTCACTT 2820
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Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTAAAGAAACAAATGCCAAAGTCACTT 2820
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QY 3001 ACAGAACTGGAATCATTTACTCCAAATTAACATGGAATTTTAAACCAATATCGAATAC 3060
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Db 3001 ACAGAACTGGAATCATTTACTCCAAATTAACATGGAATTTTAAACCAATATCGAATAC 3060
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QY 3121 AAAAATTTAGGAACATTCATGTCCTGAAAGAGAAATGGAAATGAGAAATTCCTCA 3180
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QY 3181 GTACAGTGACACAAATTACCCGTAATTAACATTAGAGAAATGTTTTTAAAGAACCGCT 3240
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| | | | |
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QY 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTACAGAGAGGATACCATGTC 4320
| | | | |

POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-3

Query Match 100.0%; Score 5711; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCTCGTGAAGTCTCTGACCCCGACAGAGCTGCGGTTCTTCAGATTAATGAGCC 60
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DB 841 CCAATTAATTAATTTGAACAACAACAGAGAGGCTGAGAGGCAATCCAGAAAGT 900
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QY 1921 ACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 1980
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QY 1981 ATGAGCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 2040
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DB 5521 GCACAGAGTTCACCCCAATTTGTTGTTGTCAGAGCAGATGCTTGAAGAGAGAGAGAG 5580
QY 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGACCCGAGAGAGAGAGAGAG 5640
DB 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGACCCGAGAGAGAGAGAGAG 5640
QY 5641 GTGTAGCACTTACACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
DB 5641 GTGTAGCACTTACACAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
QY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711

RESULT 3
US-09-074-476-5
; Sequence 5, Application US/09074476
; Patent No. 6130322
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antoinette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Thurber, Denise
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRC1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N. W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,476
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/074,453
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 5371.34.US01
; TELEPHONE: 650-463-8109
; TELEFAX: 650-463-8400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs

TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om13)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-5

Query Match 100.0%; Score 5711; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCTGCTGAGACTTCTGAGACCCCGACACAGGCTGTGGGTTTCTCAGATAAATGCGGCC 60
QY 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAGTTCATTGGAACAGAAAGAA 120
DB 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAGTTCATTGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTGGCGTTGAAGATGCAATAATGCTAATATGCTATGCAAGAAA 180
DB 121 TGGATTATCTGCTCTTGGCGTTGAAGATGCAATAATGCTAATATGCTATGCAAGAAA 180
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DB 181 TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC 240
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DB 301 GTCCCTTATGTAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACAGATTTAGTC 360
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DB 361 AACTTGTGAAAGGCTATTTGAATATCATTTTGTGCTTTTCACTTGAACACAGTTTGGAGT 420
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QY 601 CTGTGAGAACTGTGAGAACAAAGACGCGATCAACCTCAAAAGAGTGTGCTTACATG 660
DB 601 CTGTGAGAACTGTGAGAACAAAGACGCGATCAACCTCAAAAGAGTGTGCTTACATG 660
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DB 661 AATTGGAGTCTGATCTTCTGAAGATACCGTTAATTAAGCAACTTAATTCAGTGTGGAG 720
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DB 721 ATCAAGAAATTTGTAACAATCACCCCTCAAGGAAACCGGATGAATCACTTTGGATCTG 780
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DB 781 CAAAAAAGGCTGCTGTGATTTTCTGAGACGAGATGTAACAATATCTGAACATCATCAAC 840
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DB 901 ATCAGGGTATGTTCTTTCCTTCAAACTTGCATGTGAGACCATGTGAGCAAAATCTATGCCA 960
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DB 1021 AGGCTGAATTTCTGTATATTAAGAAACAGGCTGCTTGAAGAGAGCCCAATTAACAGAT 1080
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DB 1201 CAGAGAAATCTAGAGATATCTGAAGATGTTCTTGGATTAACAATAATAGCAGATTGAGA 1260
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QY 1321 GGGAGTCTGATCAAAATCCCAAAGTAGCTGATGATGAGAGCTTAAATAGTAGATGATG 1380
DB 1321 GGGAGTCTGATCAAAATCCCAAAGTAGCTGATGATGAGAGCTTAAATAGTAGATGATG 1380
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DB 1501 TTGGGAAAACTATGGAAGAAAGGCAAGCCTCCCACTTAAGCATGTAAGTAAATC 1560
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DB 1621 AATTAAACGTTAAAGAGACCTTACATGAGGCTTCAATCCGAGAGATTTTATCAAGAAAG 1680
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DB 1681 CAGATTTGGCAGTTCAAAAGACTCCTGGAATGATTAATCAAGGGAATTAACCAAGAGC 1740
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QY 1801 CTATTCAGAAATGAGAAAAATCTCTAACCAGATTAATCACTGAGAAAGAAATCTGCTTCA 1860
DB 1801 CTATTCAGAAATGAGAAAAATCTCTAACCAGATTAATCACTGAGAAAGAAATCTGCTTCA 1860
QY 1861 AAACGAAAGCTGAACCTTAAGCAGAGATTAACCAATATGGAATCTGAATTAATATCC 1920
DB 1861 AAACGAAAGCTGAACCTTAAGCAGAGATTAACCAATATGGAATCTGAATTAATATCC 1920
QY 1921 ACAATTCAAAAGACCTTAATAAGATGAGCTGAGAGAGAGTCTTCTTACAGGCAATATTC 1980
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D 1921 ACAATTCAGAGCCTTAAAGAAATAGCTGAGAGAAAGCTTTCTACAGGCAATATTC 1980
Q 1981 ATGGCTTGAAGTATGATGATGAATCTAAGCCCACTAAATGTAATGCAAA 2040
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Q 2041 TTGATGTTGTTCTAGAGTGAAGATGAAGAAAAAAGTACAAACCAATGCCAGTCA 2100
D 2041 TTGATGTTGTTCTAGAGTGAAGATGAAGAAAAAAGTACAAACCAATGCCAGTCA 2100
Q 2101 GGCACAGCAGAAACCTTCAACTCATGAGATGAAGAACTCGCACTGAGGCCAGAGAA 2160
D 2101 GGCACAGCAGAAACCTTCAACTCATGAGATGAAGAACTCGCACTGAGGCCAGAGAA 2160
Q 2161 GTACACAGCCAAATGAAGCAGACAGTAAAGACATGACAGGATCTTCTCCAGAGTGA 2220
D 2161 GTACACAGCCAAATGAAGCAGACAGTAAAGACATGACAGGATCTTCTCCAGAGTGA 2220
Q 2221 AGTTAACAAATGACCTGCTTTCTTTTAACTAAGTGTTCAAATACCAAGTGAAT 2280
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Q 2281 TTGTCAATCTTACCTTCCAGAGAGAGAAAAAGAGAACTTGAACCTGTTAAAGTGT 2340
D 2281 TTGTCAATCTTACCTTCCAGAGAGAGAAAAAGAGAACTTGAACCTGTTAAAGTGT 2340
Q 2341 CTATATATGCTGAAGACCCCAAGATCTCATGTTTAAAGTGAAGAGGTTTGCAGACTG 2400
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Q 2401 AAAGATCTGAGAGATGAGATGATTTTCAATGCTGCTGATGATGATGATGATGATGATG 2460
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Q 2461 AAAGTATCTGCTTACTGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 2520
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Q 2521 GTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
D 2521 GTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
Q 2581 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640
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Q 2641 GGGAAACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
D 2641 GGGAAACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
Q 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCAAGAGAG 2760
D 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCAAGAGAG 2760
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Q 2941 ATGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
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Q 3001 ACAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
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D 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAAGAAAAATCTGTAAGG 3120
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D 3241 CAAGCAATATTAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3300
Q 3301 TAGGTTCCAGTGAAGAACATTCAGAGAACATGATGATGATGATGATGATGATGATGATG 3360
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D 3421 GTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3480
Q 3481 ATACAGATTTCTCTCCATATCTGATTTTCAATTAAGTGAAGAACAGCTATGAGAGTATG 3540
D 3481 ATACAGATTTCTCTCCATATCTGATTTTCAATTAAGTGAAGAACAGCTATGAGAGTATG 3540
Q 3541 ATACAGATTTCTCTCCATATCTGATTTTCAATTAAGTGAAGAACAGCTATGAGAGTATG 3600
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Q 3601 AAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660
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Q 3841 CTACTAGGATGACACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 3900
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5161 CTGAAGAGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT 5220
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5701 TCAATGAGAGAGAGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT 5760
5701 TCAATGAGAGAGAGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGAAT 5760

RESULT 4
US-08-658-322-1
Sequence 1, Application US/08658322
Patent No. 5869245
GENERAL INFORMATION:
APPLICANT: Yeung, Anthony T.
TITLE OF INVENTION: Mismatch Endonuclease And Its Use in
TITLE OF INVENTION: Identifying Mutations In Targeted Polynucleotide Strands
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,322
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant

MOLECULE TYPE: DNA (genomic)
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
US-08-658-322-1

Query Match 100.0%; Score 5709.4; DB 2; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGTGAAGCTTCTGACCCCGGACACAGGCTGTGGGTTTCTAGTAATCTGGGCC 60
DB 1 AGCTCGTGAAGCTTCTGACCCCGGACACAGGCTGTGGGTTTCTAGTAATCTGGGCC 60
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DB 421 ATGCAAAACAGCTAATTTTGAAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480
QY 481 AAGTTTCTATCCAAAGATGAGGCTACAGAAACCGTCCAAAGACCTTCAAGAGTG 540
DB 481 AAGTTTCTATCCAAAGATGAGGCTACAGAAACCGTCCAAAGACCTTCAAGAGTG 540
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DB 601 CTGTGAGAACTCTGAGAGCAAGAGGATCAAACTCAAAAGACGTCTGTACATTG 660
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DB 841 CCGATATATATGATTGAACACCACTGAGAGGCTGAGAGGCACTCCAGAAAGT 900
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QY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711

RESULT 5
US-08-603-753D-1
; Sequence 1, Application US/08603753D
; Patent No. 5891857
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CELIA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,753D
; FILING DATE: 20 FEB 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/373,799
; FILING DATE: 17 JAN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383

TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5712
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHEICAL: no
: ANTI-SENSE: no
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: INDIVIDUAL ISOLATE:
: DEVELOPMENTAL STAGE: adult
: TISSUE TYPE: female breast
: CELL TYPE: ductal carcinoma in situ, invasive
: CELL LINE: breast cancer and normal breast tissue
: CELL LINE: not derived from a cell line
: ORGANELLE: no
: IMMEDIATE SOURCE:
: LIBRARY: cDNA library derived from human
: CLONE: obtained using published sequence
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: unknown
: MAP POSITION: unknown
: UNITS: unknown
: FEATURE:
: NAME/KEY: BRCA1
: LOCATION: Genbank accession no. U14680
: IDENTIFICATION METHOD: microscopically directed
: IDENTIFICATION METHOD: sampling and nuclease protection assay
: OTHER INFORMATION: gene encoding BRCA1 protein
: PUBLICATION INFORMATION:
: AUTHORS: Miki, Y., et. al.
: TITLE: A strong candidate gene for the breast and
: TITLE: ovarian cancer susceptibility gene BRCA1.
: JOURNAL: Science
: VOLUME: 266
: PAGES: 66-71
: DATE: 1994
: RELEVANT RESIDUES IN SEQ ID NO: 1:
: US-08-603-753D-1

Query Match 100.0%; Score 5709.4; DB 2; Length 5712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1021 AGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTGAAGAGGCCAATTAACAT 1080
QY 1081 GGGCTGGAAGTGAAGAAATGTAATGATAGCGGATCTCCAGACAGAAAAAGTATG 1140
DB 1081 GGGCTGGAAGTGAAGAAATGTAATGATAGCGGATCTCCAGACAGAAAAAGTATG 1140
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGATGGAATGAGAGAACTGCGATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGATGGAATGAGAGAACTGCGATGCT 1200
QY 1201 CAGAGAACTCTAGAGATCTGAGATGTTCTTGGATTAACAATAATAGCAGATTGAGA 1260
DB 1201 CAGAGAACTCTAGAGATCTGAGATGTTCTTGGATTAACAATAATAGCAGATTGAGA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGAACTGTTAGTTGCTGATGATCAATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGATGAACTGTTAGTTGCTGATGATCAATGATG 1320
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DB 1321 GGGAGTCTGAATCAAAATGCAAGAGTGTATGAGAGCTTCTAATAGGTAGATG 1380
QY 1381 AATATTTGCTTCTTCAAGAGAAATAGACTTACTGCGCAGATCTCATAGGCTTTAA 1440
DB 1381 AATATTTGCTTCTTCAAGAGAAATAGACTTACTGCGCAGATCTCATAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTGAAGATTAATTTGAAGACAAATAT 1500
DB 1441 TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTGAAGATTAATTTGAAGACAAATAT 1500

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Db	1501	TTGGGAAAAACCTATGTGGAAGAAAGGCAAGCTCTCCCACTTAAAGCATGTAACTGAAAATC	1560
QY	1561	TAAATTATAGAGCACTTGTGTACTGAGCCACAGATTAATCAAGAGCGTCCCTCCAAATA	1620
Db	1561	TAAATTATAGAGCACTTGTGTACTGAGCCACAGATTAATCAAGAGCGTCCCTCCAAATA	1620
QY	1621	AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTTCATCTGAGATTTTATCAAGAAAG	1680
Db	1621	AATTAAAGCGTAAAGAGAGACCTACATCAGGCTTTCATCTGAGATTTTATCAAGAAAG	1680
QY	1681	CAGATTTGGCGAGTTCAAAAAGACTCCTGAAATAGATTAATACAGAGAACTAACCAAGGAGC	1740
Db	1681	CAGATTTGGCGAGTTCAAAAAGACTCCTGAAATAGATTAATACAGAGAACTAACCAAGGAGC	1740
QY	1741	AGAAATGCTCAAGTGTATGATATATTAATAATAGTGTCAATGAGAAATTAACAAAGGTGATT	1800
Db	1741	AGAAATGCTCAAGTGTATGATATATTAATAATAGTGTCAATGAGAAATTAACAAAGGTGATT	1800
QY	1801	CTATTCAAGATGAGAAAAATCTTAACCAATATGAATCACTGAAAAAGATCTGCTTTCA	1860
Db	1801	CTATTCAAGATGAGAAAAATCTTAACCAATATGAATCACTGAAAAAGATCTGCTTTCA	1860
QY	1861	AAACGAAAGCTGGAACCTTAATTAAGCAGCAGATTAAGCAATATGAAATCGAAATTAATATCC	1920
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QY	1921	ACAATTTCAAAAGCACCTTAATAAGATAGGCTGAGAGGAGAACTTTCTACAGGCATATTC	1980
Db	1921	ACAATTTCAAAAGCACCTTAATAAGATAGGCTGAGAGGAGAACTTTCTACAGGCATATTC	1980
QY	1981	ATGGGCTTGAAGCTAGTACTGATGTAATCTTAAGCCCACTAAATTTGATCTGAATTTGAAA	2040
Db	1981	ATGGGCTTGAAGCTAGTACTGATGTAATCTTAAGCCCACTAAATTTGATCTGAATTTGAAA	2040
QY	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTATACCAATATGCACTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTATACCAATATGCACTCA	2100
QY	2101	GGCACAGAGAAAACCTACACTCATGTGAAGTAAAGAACTTGCAACTGAGCCAAAGAA	2160
Db	2101	GGCACAGAGAAAACCTACACTCATGTGAAGTAAAGAACTTGCAACTGAGCCAAAGAA	2160
QY	2161	GTAACAAGCCCAATATGAACAGACAAGTAAAGAAACATGACAGGATATCTTCCACAGCTGA	2220
Db	2161	GTAACAAGCCCAATATGAACAGACAAGTAAAGAAACATGACAGGATATCTTCCACAGCTGA	2220
QY	2221	AGTTAAACAATGCACTTGTTCTTTTACTTAAGTGTTCAAATATCCAGTGAACCTTAAAGAT	2280
Db	2221	AGTTAAACAATGCACTTGTTCTTTTACTTAAGTGTTCAAATATCCAGTGAACCTTAAAGAT	2280
QY	2281	TTTGCAATCCCTAGCTTCCCAAGAGAAAGAAAAAGAGAAACTTGAAGAACTTAAAGTGT	2340
Db	2281	TTTGCAATCCCTAGCTTCCCAAGAGAGAAAGAAAAAGAGAAACTTGAAGAACTTAAAGTGT	2340
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Db	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTGTTAAGTGAAGAAAGGGTTTGCAAACTG	2400
QY	2401	AAAGATCTGTAGAGATGACGATATTTCAATGGTACCTGGTATCAAGATTAATGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGATGACGATATTTCAATGGTACCTGGTATCAAGATTAATGCACTCAGG	2460
QY	2461	AAAGATCTGTACTGGAAGTTTAGCACTTAGGGAAGGCAAAACAGAACTAATTAAT	2520
Db	2461	AAAGATCTGTACTGGAAGTTTAGCACTTAGGGAAGGCAAAACAGAACTAATTAAT	2520
QY	2521	GTGTGAGTCAAGTGTGACAGACTTTGAAAAACCCCAAGGACCTAATTCATGCTTTGTTCAAG	2580
Db	2521	GTGTGAGTCAAGTGTGACAGACTTTGAAAAACCCCAAGGACCTAATTCATGCTTTGTTCAAG	2580

QY	2551	TTAAATGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAAGTTAAACAAGCTC	264
Db	2551	ATAAATGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAAGTTAAACAAGCTC	264
QY	2641	GGGAAACAGACATAGAAATGGAAGAAGTGAATCTGATGCTAGATTTGGAGAAATACAT	2700
Db	2641	GGGAAACAGACATAGAAATGGAAGAAGTGAATCTGATGCTAGATTTGGAGAAATACAT	2700
QY	2701	TCAAAGTTCAAAGGCGCCAGTCATTGGCTCTGTGTTTCAATCCAGAAATGCAGAAAGG	2760
Db	2701	TCAAAGTTCAAAGGCGCCAGTCATTGGCTCTGTGTTTCAATCCAGAAATGCAGAAAGG	2760
QY	2761	AATGTCACAATCTCTGCGCCACTCTGGGTCTTAAAGAAAACAAAGTCCAAAGTCACTT	2820
Db	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATGACTCTAATTCAAAGCTGAC	2880
QY	2881	AGACAGTTAATATCACTGCAGAGCTTCCCTGTGTGGTGCAGAAAATAGCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGCAGAGCTTCCCTGTGTGGTGCAGAAAATAGCAGTTGATA	2940
QY	2941	ATGCCAAATGATGATCAAGAGAGCTTAGGTTTGTCTATCTCATTCAAGTCCAGAGCA	3000
Db	2941	ATGCCAAATGATGATCAAGAGAGCTTAGGTTTGTCTATCTCATTCAAGTCCAGAGCA	3000
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Db	3001	ACGAAACCTGAGCTCAATTAATCCAAATAAACATGGAATCTTTTCAAAACCCATATGATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCATTTGTTAAACATTAATGTAAAGAAAATGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCATTTGTTAAACATTAATGTAAAGAAAATGCTAGAGG	3120
QY	3121	AAAACTTTGAGAAACATTCAAATGTCACCTGAAAGAAATGGAAATGAGAACTTCCAA	3180
Db	3121	AAAACTTTGAGAAACATTCAAATGTCACCTGAAAGAAATGGAAATGAGAACTTCCAA	3180
QY	3181	GTAACAGTACGACAAATTAGCCGTAAATACATTAAGAAAAATGTTTTTAAGAACCCAGCT	3240
Db	3181	GTAACAGTACGACAAATTAGCCGTAAATACATTAAGAAAAATGTTTTTAAGAACCCAGCT	3240
QY	3241	CAAGCAATATTAAGAAGTAGTTCACAGTACTAATGAAGGGGCTCCAGTTTAATGAAA	3300
Db	3241	CAAGCAATATTAAGAAGTAGTTCACAGTACTAATGAAGGGGCTCCAGTTTAATGAAA	3300
QY	3301	TAGGTTCCAGTATGAAAAACATTCACAGCAAACTAGGTAGAAACAGAGGGCCAAAAATGGA	3360
Db	3301	TAGGTTCCAGTATGAAAAACATTCACAGCAAACTAGGTAGAAACAGAGGGCCAAAAATGGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTGGCAACTGAGGTCCTATAAACAAAGCTTCTCGAAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTGGCAACTGAGGTCCTATAAACAAAGCTTCTCGAAA	3420
QY	3421	GTAATTTGAAGCAATCCGGAATTAAGAAAGCAAGAAATGGAAGATGATCAGACTGTTA	3480
Db	3421	GTAATTTGAAGCAATCCGGAATTAAGAAAGCAAGAAATGGAAGATGATCAGACTGTTA	3480
QY	3481	ATACAGATTTCTCCATATCTGATTTTCAGATTAATTAGAAACAGCTCTATGGGAAGTATGC	3540
Db	3481	ATACAGATTTCTCCATATCTGATTTTCAGATTAATTAGAAACAGCTCTATGGGAAGTATGC	3540
QY	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGAATTAAGG	3600
QY	3601	AAGATACAGTTTGTCTGAAAATGACATTAAGGAAATGTCGCGTCTTTTAGCAAAAAGCG	3660
Db	3601	AAGATACAGTTTGTCTGAAAATGACATTAAGGAAATGTCGCGTCTTTTAGCAAAAAGCG	3660
QY	3661	TCGAGAAAGGAGACTTAGCAGAGTCTTAGCCCTTTCACCCATACATTTGGCTAGG	3720

APPLICANT: JENSEN, ROY A.
 APPLICANT: PAGE, DAVID L.
 APPLICANT: KING, MARY-CLAIRE
 APPLICANT: SZABO, CSILLA I.
 APPLICANT: JETTON, THOMAS L.
 APPLICANT: ROBINSON-BENION, CHERYL L.
 APPLICANT: THOMPSON, MARILYN E.
 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
 TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARLES A. TAYLOR, JR.
 STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
 STREET: BOULEVARD
 CITY: DURHAM
 STATE: NORTH CAROLINA
 COUNTRY: USA.
 ZIP: 27707
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
 COMPUTER: IBM PC/XT/AT compatible
 OPERATING SYSTEM: Windows 3.1
 SOFTWARE: WORD PERFECT 6.1 and ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,753
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/603,753
 FILING DATE: 20 FEB 1996
 APPLICATION NUMBER: U.S. 08/373,799
 FILING DATE: 17 JAN 1995
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 TELEPHONE: (919) 493-8000
 TELEFAX: (919) 419-0383
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5712
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: no
 ANTI-SENSE: no
 IMMEDIATE SOURCE:
 ORGANISM: Homo sapiens
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE: adult
 TISSUE TYPE: female breast
 CELL TYPE: ductal carcinoma in situ, invasive
 CELL TYPE: breast cancer and normal breast tissue
 CELL LINE: not derived from a cell line
 ORGANELLER: no
 IMMEDIATE SOURCE:
 LIBRARY: cDNA library derived from human
 CLONE: obtained using published sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: unknown
 MAP POSITION: unknown
 UNITS: unknown
 FEATURE:
 NAME/KEY: BRCA1
 LOCATION: GenBank accession no. U14680
 IDENTIFICATION METHOD: microscopically directed
 IDENTIFICATION METHOD: sampling and nuclease protection assay
 OTHER INFORMATION: gene encoding BRCA1 protein
 PUBLICATION INFORMATION:

Query Match	Best Local Similarity	100.0%	Score 5709.4	DB 3	Length 5712
Matches 5710	Conservative	0	Mismatches	1	Indels
					Gaps
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QY	5701	GCCACTACTGGA 5711	
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INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
US-08-986-106-1

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Db 5701 GCCACTACTGA 5711

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RESULT 8

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US-09-007-678B-47
; Sequence 47, Application US/09007678B
; Patent No. 6342483
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: OBERMILLER, PATRICE S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2
; CURRENT APPLICATION NUMBER: US/09/007,678B
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 08/373,799
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 08/182,961
; PRIOR FILING DATE: 1994-01-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO 47
; LENGTH: 5712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (120)..(5708)

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; NAME/KEY: misc feature
; LOCATION: (4532)..(4535)
; OTHER INFORMATION: Xaa-any amino acid
US-09-007-678B-47
Query Match 100.0%; Score 5709.4; DB 4; Length 5712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 601 CTGTGAGACTGTGAGAGCAAGAGCAGGATCAACCTCAAAAAGAGCTGTGTACATTTG 660
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Db 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATGCAAGTGGAG 720
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Db 781 CAAAAAGGCTGTTGTAATTTTCTGAGACGGAATTAACAATATGTAACATCAATCAAC 840
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Db 841 CAGTATATATGATTTGAACACCACTGAGAACGCTGACGTAGAGGATCCAGAAAGT 900
QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGACATGTGAGAGCATGTGGCACTCAATGATGCA 960
Db 901 ATCAGGGTATGTTCTGTTTCAAACTTGACATGTGAGAGCATGTGGCACTCAATGATGCA 960

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QY 961 GCTCATTCAGCATGAGAAACAGCAGTTTATTACTCACTAAAGCAGAAATGAATGTGAAA 1020
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DB 1021 AGGCTGAATTCGTATTAATAAGCAACAGCCTGGCTTAGCAAGAGCCCAACATACAGAT 1080
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DB 1081 GGGCTGGAAGTAAGGAAACATGTATGATAGCGGAGCTCCAGCAGACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATAGAAATAGCAAGAACTGCCAGCT 1200
DB 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATAGAAATAGCAAGAACTGCCAGCT 1200
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QY 1321 GGGAGCTGAATCAATGCCAAAGTAGCTGATGTTGAGCGTTCTAAATAGAGATGATG 1380
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DB 1681 CAGATTTGGCAGTTCAAAAAGACTCTGAATGATTAATCAAGGAACTTAACCAACGAGC 1740
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DB 1741 AGAATGTCAGATGATTAATTAATTAATAGTGTCTATGAGAAATTAACAAAGGTGAT 1800
QY 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGCTTCA 1860
DB 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGCTTCA 1860
QY 1861 AAACGAAAGCTGAACCTATAGCAGCAGATTAAGCAATATGAACTGAAATTAATATCC 1920
DB 1861 AAACGAAAGCTGAACCTATAGCAGCAGATTAAGCAATATGAACTGAAATTAATATCC 1920
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DB 2221 AGTTAAACAATGACACCTGTTCTTTTACTAAAGTGTCAATTAACAGTAACTTAAAGAT 2280
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DB 2281 TTGTCAATCTTACGCTTCCAGAGAAAGAAAGAGAACTGAAACATTAAGTGT 2340
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DB 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTCGAACTG 2400
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Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAAGAGAGATGTG 5340

QY	5341	CCATGGAAGAAACACACCAAGAGTCCAAAGCGACGAAGAAGATGCCAGGACAGAAAGATCT	5400
Db	5341	TCAATTGGAGAGAAACCAACCAAGAGTCCAAAGCGACGAAGAAGATGCCAGGACAGAAAGATCT	5400
QY	5401	TCAGGGGGGCTTGAAATCTGTGCTATGAGGCCCTTCACCAACATGCCACAGATCAACTGG	5460
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QY	5461	AATGGATGTGTACAGCTGTGTGTGCTTTCTGTGTGTGAAGAGACTTTTCATCATTCACCTTG	5520
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QY	5521	GCACAGGTGTCAACCCCAATTGGTGTGTGACGACAGATGCTGTGACAGAGACAATGGCT	5580
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QY	5581	TCCATGTCAATTGGGCGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
Db	5581	TCCATGTCAATTGGGCGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
QY	5641	GTTGTAGCACTCTACCAAGTCCAGGAGCTGTGACACTTACTGATACCCCAATCCCCCACA	5700
Db	5641	GTTGTAGCACTCTACCAAGTCCAGGAGCTGTGACACTTACTGATACCCCAATCCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	

RESULT 9
 US-08-480-784-1
 Sequence 1, Application US/08480784
 Patent No. 5693473
 GENERAL INFORMATION:
 APPLICANT: Skolnick, Mark H.
 APPLICANT: Goldgar, David E.
 APPLICANT: Miki, Yoshio
 APPLICANT: Swenson, Jeff
 APPLICANT: Kamb, Alexander
 APPLICANT: Harshman, Keith D.
 APPLICANT: Shatruck-Eldens, Donna M.
 APPLICANT: Tavtighian, Sean V.
 APPLICANT: Wiseman, Roger W.
 APPLICANT: Futreal, P. Andrew
 TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
 TITLE OF INVENTION: Susceptibility Gene
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESS: Verable, Baetjer, Howard & Civiletti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,784
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/409,305
 FILING DATE: 24-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,824
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,104
 FILING DATE: 16-SEP-1994
 PRIOR APPLICATION DATA:

	APPLICATION NUMBER:	US 08/300,266
	FILING DATE:	02-SEP-1994
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER:	US 08/289,221
	FILING DATE:	12-AUG-1994
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Ihren, Jeffrey L.
	REGISTRATION NUMBER:	28,957
	REFERENCE/DOCKET NUMBER:	24884-109347
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	202-962-4810
	TELEFAX:	202-962-8300
	INFORMATION FOR SEQ ID NO:	1:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	5914 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	double
	TOPOLOGY:	linear
	MOLECULE TYPE:	cDNA
	HYPOTHETICAL:	NO
	ANTI-SENSE:	NO
	ORIGINAL SOURCE:	
	ORGANISM:	Homo sapiens
	FEATURE:	
	NAME/KEY:	CDS
	LOCATION:	120..5711
	US-08-480-784-1	
QY	Query Match	100.0%; Score 5709.4; DB 1; Length 5914;
Db	Best Local Similarity	100.0%; Pred. No. 0;
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RESULT 10

US-08-483-553-1
; Sequence 1, Application US/08483553
; Patent No. 5709999
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldfar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshe, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavel, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,553
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
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TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: 120..5711
US-08-483-553-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	3301	TAGGTTCCAGTATGAAAAACATTCAAGCAGAACTAGTGAAGAACAGAGGCGCAAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAAAACATTCAAGCAGAACTAGTGAAGAACAGAGGCGCAAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGGCTATATPAAACAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGGCTATATPAAACAAGTCTTCTGGAA	3420
QY	3421	GTAATTTGAACATCTCGAATTAATAAAGCAAGATATGAAGAAAGTAGTTCAAGCTGTTA	3480
Db	3421	GTAATTTGAACATCTCGAATTAATAAAGCAAGATATGAAGAAAGTAGTTCAAGCTGTTA	3480
QY	3481	ATAACAGATTTCTCTCATATCTGAATTTGAGATACTTGAACAGGCTATGAGGAAGTAGTC	3540
Db	3481	ATAACAGATTTCTCTCATATCTGAATTTGAGATACTTGAACAGGCTATGAGGAAGTAGTC	3540
QY	3541	ATGCATCTCAGGTTGTTTCTGAAGACCTGATGACCTGTTAGATGATGAGTAAGTAAG	3600

Db	3541	ATGCACTCAGAGTTTGTTCTGAGACACTGTAAGACCTGTATAGATGATGTAATAAAGG	3600
Qy	3601	AAGATATAGATTGTCGTAAAAATGACATTAAGAAAGTTTCGTGTTTTAGCAAAACG	3660
Db	3601	AAGATACTAGTTTCTGTAAATATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACG	3660
Qy	3661	TCAGAAAGAGAGCTTAGCAGAGAGTCTAGGCCCTTACCCCATACACATTTGGCTCAG	3720
Db	3661	TCAGAAAGAGAGAGCTTAGCAGAGAGTCTAGGCCCTTACCCCATACATTTGGCTCAG	3720
Qy	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGACATTAATCTAGTGAAGT	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGACATTAATCTAGTGAAGT	3780
Qy	3781	AAGAGCTTCCCGCTCCCAACTGTGTAATTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCGCTCCCAACTGTGTAATTGGTAAAGTAAACAATATATCCTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCGGTGCTACCGAGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGGTGCTACCGAGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTGAAGATATAGCTTAATATGATCTGCAGTAACCAAGTATATTTGGCAAAAGCATTC	3960
Db	3901	TATCATTTGAAGATATAGCTTAATATGATCTGCAGTAACCAAGTATATTTGGCAAAAGCATTC	3960
Qy	3961	AGGAACATCACCTTAGTAGAGGAAACAAATGTCGTAGCTGTTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGGAAACAAATGTCGTAGCTGTTTTCTTCACAGTCA	4020
Qy	4021	GTGAATTGGAAGACTGACCTGCAAAATACAAACCCAGAGTCTTTCTTGAATGGTCTT	4080
Db	4021	GTGAATTGGAAGACTGACCTGCAAAATACAAACCCAGAGTCTTTCTTGAATGGTCTT	4080
Qy	4081	CCAAACAATAGGCATATGTTCTGAAAGCCAGGAGTTGGTCTGATGTAACAAGATTGG	4140
Db	4081	CCAAACAATAGGCATATGTTCTGAAAGCCAGGAGTTGGTCTGATGTAACAAGATTGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAAAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAAAGCAAGCA	4200
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Db	4201	TGGAATTCMAATTAGTAGTGAAGCAGCATCTGGGTTGAGAGTGAACAAGCCTCTCTGAG	4260
Qy	4261	ACTGCTCAGGGCTATTCCTCTCAGAGTGAATTTAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATTCCTCTCAGAGTGAATTTAACCACTCAGCAGAGGATACCATGC	4320
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Db	4381	ATGGAGGACGACCTTCTTAACAGTACCTTCATATAAGTGACTCTTCTGAGG	4440
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Qy	4501	GTGAATACCCCTATTAAGCCAGATATCCAAAGGCTTTTGCTGACAAAGTTTGAAGGTCTG	4560
Db	4501	GTGAATACCCCTATTAAGCCAGATATCCAAAGGCTTTTGCTGACAAAGTTTGAAGGTCTG	4560
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Db	4561	CAGATATGTTCTACACAGTAAAAATTAAGAACACAGAGTGAAGAAAGTCAATCCCTCTTAAT	4620
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Db		4621	GCCCATCAATTGATGATAGTGTGGTCATGCACAGTTGCTTGCGGAGTCTTCAGAAATAGAA	4680
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OY		4861	AAGACAGAGCCCACAGATCAGCTCGTGTGGCACATACCATCTTCAAACCTCTGATTTGA	4920
Db		4861	AAGACAGAGCCCCACAGATCAGCTCGTGTGGCACATACCATCTTCAAACCTCTGATTTGA	4920
OY		4921	AAGTTCGCCCAATTGGAAGTTGAGAAATCTGCCAACAGTCCAGCTGCTCTCATCTACTG	4980
Db		4921	AAGTTCGCCCAATTGGAAGTTGAGAAATCTGCCAACAGTCCAGCTGCTCTCATCTACTG	4980
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Db		4981	ATACTGCTGGGATATATGCAATGGAAGAAAGTGTGAGAGAGGAGAGACCAAAATTGACAG	5040
OY		5041	CTTCAACAGAAAGGCTCAACAAAGATGTCCATGCTGTGCTTGCCCTGACCCCAAGAG	5100
Db		5041	CTTCAACAGAAAGGCTCAACAAAGATGTCCATGCTGTGCTTGCCCTGACCCCAAGAG	5100
OY		5101	AATTATGCTGTGACAAAGTTGGCCAGAAAAACACATCATCTTAATCTAATTA	5160
Db		5101	AATTATGCTGTGACAAAGTTGGCCAGAAAAACACATCATCTTAATCTAATTA	5160
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Db		5161	CTGAAGAGACTACTATGTTGTTATGAAGAAACAGATGCTGAGTTGTGTGTGAACGCAAC	5220
OY		5221	TGAAATATTTTTCTAGAAATTCGGGAGAGAAATGGGTAGTTACTATTTCTGGGTGACCC	5280
Db		5221	TGAAATATTTTTCTAGAAATTCGGGAGAGAAATGGGTAGTTACTATTTCTGGGTGACCC	5280
OY		5281	AGCTATTTAAAGAAAGAAAAAGCTCGAATGAGCATGATTTTGAAGTCAGAGAGAGATGGG	5340
Db		5281	AGCTATTTAAAGAAAGAAAAAGCTCGAATGAGCATGATTTTGAAGTCAGAGAGAGATGGG	5340
OY		5341	TCAATGGAAGAAACCACCAAGGTCGAAAGCGAGCAAGAAATCCCAAGACAGAAAGATCT	5400
Db		5341	TCAATGGAAGAAACCACCAAGGTCGAAAGCGAGCAAGAAATCCCAAGACAGAAAGATCT	5400
OY		5401	TCAGGGGGCTAGAAAATCTGTGCTATGggcccttaccacaaatgcccacagatcaactgg	5460
Db		5401	TCAGGGGGCTAGAAAATCTGTGCTATGggcccttaccacaaatgcccacagatcaactgg	5460
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Db		5461	AATGATGGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGCTTTCATCATCTTCAACCTTG	5520
OY		5521	GCACAGGTGTCCACCCAATTGCTGTGTGACGACGATGCGCTCGACCAAGAGCAATGGCT	5580
Db		5521	GCACAGGTGTCCACCCAATTGCTGTGTGACGACGATGCGCTCGACCAAGAGCAATGGCT	5580
OY		5581	TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGTACCCGAGAGTGGGTGTTGACA	5640
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OY		5641	GTTGACACTTACCAAGTGCACAGAGCTGGACACTTACCTGATACCCAGATCCCCACA	5700
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Db		5701	GCCACTACTGCA 5711	

```

RESULT 11
US-08-487-002-1
: Sequence 1, Application US/08487002
: Patent No. 5710001
: GENERAL INFORMATION:
: APPLICANT: Shattuck-Eidens, Donna M.
: APPLICANT: Simard, Jacques
: APPLICANT: Emi, Mitsuru
: APPLICANT: Nakamura, Yusuke
: APPLICANT: Durocher, Francine
: TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
: TITLE OF INVENTION: Susceptibility Gene
: NUMBER OF SEQUENCES: 85
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
: STREET: 1201 New York Avenue, N.W., Suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,002
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/409,305
: FILING DATE: 24-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/348,824
: FILING DATE: 29-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/308,104
: FILING DATE: 16-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/300,266
: FILING DATE: 02-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/289,221
: FILING DATE: 12-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Ihnen, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: REFERENCE/DOCKET NUMBER: 24884-109347
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-962-4810
: TELEFAX: 202-962-8300
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5914 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 120..5711
:
: US-08-487-002-1
:
: Query Match 100.0%; Score 5709.4; DB 1; Length 5914;
: Best Local Similarity 100.0%; Pred. No. 0;
: Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0

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Db 301 GTCTTTATGTAAGATGATTAACCAAAAGAGCTTACAAAGAAAGTACGAGATTTAGTC 360
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 Db 5701 GCCACTACTGA 5711

RESULT 12

US-08-483-554B-1
 Sequence 1, Application US/08483554B
 Patent No. 5747282
 GENERAL INFORMATION:
 APPLICANT: Skolnick, Mark H.
 APPLICANT: Goldger, David E.
 APPLICANT: Miki, Yoshio
 APPLICANT: Swenson, Jeff
 APPLICANT: Kamb, Alexander
 APPLICANT: Harshman, Keith D.
 APPLICANT: Shattuck-Eidens, Donna M.
 APPLICANT: Tavlijan, Sean V.
 APPLICANT: Wiseman, Roger W.
 APPLICANT: Futreal, P. Andrew
 TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
 TITLE OF INVENTION: Susceptibility Gene
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,554B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/409,305
 FILING DATE: 24-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,824
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,104
 FILING DATE: 16-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300,266
 FILING DATE: 02-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,221
 FILING DATE: 12-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109347

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5914 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 120..5708
US-08-483-554B-1

Query Match 100.0% Score 5709.4; DB 1; Length 5914;
Best Local Similarity 100.0%; Pred No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 13
US-08-488-011B-1
; Sequence 1, Application US/08488011B
; Patent No. 5753441
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shatluck-Eldens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,011B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347-09
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5914 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 120..5708
US-08-488-011B-1

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Query Match 100.0%; Score 5709.4; DB 1; Length 5914;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 421 ATGCAAAAGCTATTAATTTTGCAGAAAAGAAATTAATCTCTGAAATTAAGATG 480
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RESULT 14
 US-08-850-727-1
 ; Sequence 1, Application US/08850727
 ; Patent No. 6162897
 ; GENERAL INFORMATION:
 ; APPLICANT: Skolnick, Mark H.
 ; APPLICANT: Goldgar, David E.

APPLICANT: Miki, Yoshio
 APPLICANT: Swenson, Jeff
 APPLICANT: Kamb, Alexander
 APPLICANT: Harshman, Keith D.
 APPLICANT: Shatuck-Eldens, Donna M.
 APPLICANT: Tavtugian, Sean V.
 APPLICANT: Wiseman, Roger W.
 APPLICANT: Futreal, P. Andrew
 TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/850,727
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/483,554
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,824
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/308,104
 FILING DATE: 16-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300,266
 FILING DATE: 02-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,221
 FILING DATE: 12-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Innen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 24884-109347
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5914 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 120..5708
 US-08-850-727-1

Query Match 100.0%; Score 5709.4; DB 4; Length 5914;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACTCGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGTTTCACATACTGGCC 60
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Qy      5701  GCCACTACTGA 5711
Db      5701  GCCACTACTGA 5711

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RESULT 15
PCT-US95-10202-1

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Sequence 1, Application PC/TUS9510202
GENERAL INFORMATION:
APPLICANT: Shattuck-Bidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Emi, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Durocher, Francine
TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
TITLE OF INVENTION: In the 17q-linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10202
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5914 base pairs

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 120..5711
PCT-US95-10202-1

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Query Match 100.0%; Score 5709.4; DB 5; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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2701 TGAAGTTTCAAGAGGCGCAGTATTTGCTGCTGTTTCAAAATCGAGAAATCAGAAAGG 2760
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Qy	5341	TCATGGAAGAAACCCAGGCTCCAAAGCGAGCAAGAAATCCACAGACAGAAAGATCT	5400
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Qy	5581	TCCATGCAATTGGGAGATGTGTGAGGCACTGTGTGACCCGAGAGTGGGTGTGACA	5640
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Qy	5641	GTGTAGCACTCTACCAAGTGCAGAGACTGAGACACTTACTGATACCCAGATCCCCACA	5700
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Db	5701	GCCACTACTGA 5711	

Search completed: June 13, 2003, 12:21:43
Job time : 298 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:07:45 ; Search time 1106 Seconds
(without alignments)
11628.537 Million cell updates/sec

Title: US-09-734-672-1
Perfect score: 5711
Sequence: 1 ACCTCGCTGAGACTTCTGTG.....TCCCCACAGCAGCTACTGTA 5711

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	5711	100.0	5711	19	AAV62180
3	5711	100.0	5711	19	AAV46448
4	5711	100.0	5711	21	AAV60793
5	5710.6	100.0	5711	19	AAV46470
6	5710.6	100.0	5711	19	AAV46451
7	5710.6	100.0	5711	19	AAV46452
8	5710.6	100.0	5711	19	AAV46453
9	5710.6	100.0	5711	19	AAV46454

10	5710.6	100.0	5711	19	AAV46455
11	5710.6	100.0	5711	19	AAV46456
12	5710.6	100.0	5711	19	AAV46457
13	5709.4	100.0	5711	19	AAV46450
14	5709.4	100.0	5711	21	AAV60794
15	5709	100.0	5711	19	AAV46465
16	5709	100.0	5711	19	AAV46466
17	5709	100.0	5711	19	AAV46467
18	5709	100.0	5711	19	AAV46468
19	5709	100.0	5711	19	AAV46469
20	5709	100.0	5711	19	AAV46471
21	5702.6	99.9	5711	19	AAV46463
22	5702.6	99.9	5711	19	AAV46464
23	5702.6	99.9	5711	19	AAV46465
24	5702.6	99.9	5711	19	AAV46461
25	5702.6	99.9	5711	19	AAV46462
26	5701.4	99.8	5711	19	AAV46449
27	5701.4	99.8	5711	21	AAV60795
28	5701.4	99.8	5914	17	AAT17491
29	5701.4	99.8	5914	17	AAT17492
30	5701.4	99.8	5914	17	AAT17493
31	5701.4	99.8	5914	17	AAT17494
32	5701.4	99.8	5914	17	AAT17495
33	5701.4	99.8	5914	17	AAT17496
34	5701.4	99.8	5711	19	AAV46458
35	5701	99.8	5711	19	AAV46460
36	5699.8	99.8	5712	18	AAT84840
37	5699.8	99.8	5712	21	AAZ87995
38	5699.8	99.8	5914	17	AAT33601
39	5699.8	99.8	5914	17	AAT17438
40	5699.8	99.8	5914	17	AAT18310
41	5698.2	99.8	5711	17	AAT42024
42	5698.2	99.8	5711	17	AAT42030
43	5698.2	99.8	5711	18	AAT70067
44	5698.2	99.8	5711	18	AAT70073
45	5698.2	99.8	5711	19	AAV60563

ALIGNMENTS

RESULT 1	AAV60795	standard; cDNA; 5711 BP.
AAV60795		
AC	AAT87085;	
XX		
DT	06-JAN-1998	(first entry)
XX		
DE	Human BRCA1 gene consensus.	
KM	BRCA1 gene; BRCA1 (om1); breast cancer; ovary cancer; polymorphism;	
KW	genetic testing; diagnosis; gene therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
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FT		/*tag= b
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FT	variation	2430
FT		/*tag= c
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FT	variation	2731
FT		/*tag= d
FT		/note= "25-35% CCG (Pro) and 65-75% CTG (Leu) polymorphism at position 2731"
FT	variation	3232
FT		/*tag= e

FT /note= "35-45% GAA (Glu) and 55-65% GGA (Gly)
 FT polymorphism at position 3232"
 FT variation 3667
 FT /tag= f
 FT /note= "35-45% AAA (Lys) and 55-65% AGA (Arg)
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 FT variation 4427
 FT /tag= g
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 FT variation 4956
 FT /tag= h
 FT /note= "35-45% AGT (Ser) and 55-65% GGT (Gly)
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 PN US5654155-A.
 XX 05-AUG-1997.
 XX 12-FEB-1996; 96US-0598591.
 XX 12-FEB-1996; 96US-0598591.
 XX 12-FEB-1996; 96US-0598591.
 XX (ONCO-) ONCORMED INC.
 XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,
 PI Schelter DB, Zeng B;
 DR WPI; 1997-401843/37.
 DR P-PSDB; AAW26522.
 XX Human BRCA1 gene coding sequence with common normal polymorphisms -
 PT for assessing susceptibility to breast or ovarian cancer
 PS Claim 1; Column 19-24; 35pd; English.
 XX This nucleotide sequence comprises a consensus DNA sequence,
 CC designated BRCA1(oml), for the normal human BRCA1 gene. It was
 CC found by end-to-end sequencing of the BRCA1 gene from 5 individuals
 CC randomly drawn from the population and found to have no family
 CC history of breast or ovarian cancer. The BRCA1(oml) gene and the
 CC seven polymorphic sites (which are not associated with breast or
 CC ovarian cancer) will provide greater accuracy and reliability for
 CC genetic testing. A claimed method for detecting an increased
 CC genetic susceptibility to breast and ovarian cancer resulting from
 CC the presence of a mutation in the BRCA1 coding sequence involves
 CC amplifying and sequencing the BRCA1 coding sequence from an
 CC individual and comparing the sequence with BRCA1(oml). The
 CC consensus normal BRCA1 sequence can also be used in gene therapy,
 CC to make diagnostic probes and to express normal BRCA1 polypeptide
 CC (see AAW26522).
 XX
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;
 Query Match 100.0%; Score 5711; DB 18; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 241 ACATATTTTGAATTTTGCATGCGTGAACCTTCTCAACGAGAAAGGGCTTACAGT 300
 QY 301 GTCCCTTATGTAGATGATATTAACCAAAAGAGCCTTACAAAGAGTACGATTTAGT 360
 DB 301 GTCCCTTATGTAGATGATATTAACCAAAAGAGCCTTACAAAGAGTACGATTTAGT 360
 QY 361 AACTTGTGAAGAGTATTTGAATTCATTTGTCTTTACCTTGAACAGGTTTGAAT 420
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QY 1741 AGAATGCTCAAGTAGTAATTTACTTAATAGTGTATGATGAATTAATAAAGGATTT 1800
DB 1741 AGAATGCTCAAGTAGTAATTTACTTAATAGTGTATGATGAATTAATAAAGGATTT 1800
QY 1801 CTATTGAGATGAGAAAAATCCTAACCCAAATGAAATCACTCGAAAAAGATCTGCTTCA 1860
DB 1801 CTATTGAGATGAGAAAAATCCTAACCCAAATGAAATCACTCGAAAAAGATCTGCTTCA 1860
QY 1861 AAACGAAGCTGAACCTATTAAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920
DB 1861 AAACGAAGCTGAACCTATTAAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920
QY 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
DB 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
QY 1981 ATGCGCTTGAACCTAGTAGTCAAGTAAGTCTAAAGCCACCTAATGTAATGCAATTCGAA 2040
DB 1981 ATGCGCTTGAACCTAGTAGTCAAGTAAGTCTAAAGCCACCTAATGTAATGCAATTCGAA 2040
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCGCAGTCA 2100
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCGCAGTCA 2100
QY 2101 GGGACAGCAGAAACCTTAACTCATGGAAGTAAAGAACCTGCAATGAGCCAGAAAGA 2160
DB 2101 GGGACAGCAGAAACCTTAACTCATGGAAGTAAAGAACCTGCAATGAGCCAGAAAGA 2160
QY 2161 GTTAAAGGCAATGAAGCAAGTAAGTAAGCAATGATGATGATTTTCCAGAGCTGA 2220
DB 2161 GTTAAAGGCAATGAAGCAAGTAAGTAAGCAATGATGATGATTTTCCAGAGCTGA 2220
QY 2221 AGTTAAACAATGACCTGGTCTTTTACTTAAGTTCCTAATACAGTGAATCTTAAAGAT 2280
DB 2221 AGTTAAACAATGACCTGGTCTTTTACTTAAGTTCCTAATACAGTGAATCTTAAAGAT 2280
QY 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
DB 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
QY 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACG 2400
DB 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACG 2400
QY 2401 AAAGATCTGAGAGTAGAGATTAATTTCACTGGTACTGTAATTTGGCACTCAG 2460

DB 2401 AAAGATCTGAGAGTAGAGTAGACAGATTTTCACTGGTACTGGTACTGATTAATGACCTCAGG 2460
QY 2461 AAAGATCTGAGAGTAGAGTAGACAGATTTTCACTGGTACTGGTACTGATTAATGACCTCAGG 2520
DB 2461 AAAGATCTGAGAGTAGAGTAGACAGATTTTCACTGGTACTGGTACTGATTAATGACCTCAGG 2520
QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAAGCCCAAGGAGTAAATTCAGGTTTCCAAAG 2580
DB 2521 GTGTAGTCAAGTGTGACAGATTTGAAAGCCCAAGGAGTAAATTCAGGTTTCCAAAG 2580
QY 2581 ATTAATGAAGATGACAGAGAGCTTTAAGTATCAATGGGACATGAAGTTAAACAGTC 2640
DB 2581 ATTAATGAAGATGACAGAGAGCTTTAAGTATCAATGGGACATGAAGTTAAACAGTC 2640
QY 2641 GGGAAACAAGCATTAAGATTAAGAAAGTGAAGCTTGAATGCTCATGATTTTGGCAATACAT 2700
DB 2641 GGGAAACAAGCATTAAGATTAAGAAAGTGAAGCTTGAATGCTCATGATTTTGGCAATACAT 2700
QY 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAAAATCAGGAAATGAGAAAGAG 2760
DB 2701 TCAAGGTTTCAAGGCGCAGTCAATTTGCTGTTTCAAAATCAGGAAATGAGAAAGAG 2760
QY 2761 AATGTGCAACATTTCTGTGCCCATCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820
DB 2761 AATGTGCAACATTTCTGTGCCCATCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820
QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGAAAGTCAATATCAAGCTGTAC 2880
DB 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGAAAGTCAATATCAAGCTGTAC 2880
QY 2881 AGACAGTAAATATCACTGAGGCTTCTGTGGTGTGAGAAAGATTAAGCCAGTTGATA 2940
DB 2881 AGACAGTAAATATCACTGAGGCTTCTGTGGTGTGAGAAAGATTAAGCCAGTTGATA 2940
QY 2941 ATGCCAAATGTATGATCAAGAGAGGCTGTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000
DB 2941 ATGCCAAATGTATGATCAAGAGAGGCTGTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000
QY 3001 AGGAAATGAGATCTTACTCCAAATTAACATGAGACTTTTACAAACCATATGCTATAC 3060
DB 3001 AGGAAATGAGATCTTACTCCAAATTAACATGAGACTTTTACAAACCATATGCTATAC 3060
QY 3061 CACGACTTTTCCCATCAAGTCAATGTTTAAATGTAAGAAATGCTGATAGAG 3120
DB 3061 CACGACTTTTCCCATCAAGTCAATGTTTAAATGTAAGAAATGCTGATAGAG 3120
QY 3121 AAACTTTGAGGACATTCATGTCACTGAAAGAAATGGAATGAAACATTCGA 3180
DB 3121 AAACTTTGAGGACATTCATGTCACTGAAAGAAATGGAATGAAACATTCGA 3180
QY 3181 GTACAGTGAACCAATTTGCGGTAAATTAATGAGAAATGTTTTTAAAGAGCGAGT 3240
DB 3181 GTACAGTGAACCAATTTGCGGTAAATTAATGAGAAATGTTTTTAAAGAGCGAGT 3240
QY 3241 CAAGCAATTAATTAAGAGGTTCCAGTCAATGAAGTGGGCTCCAGTATTAATGAA 3300
DB 3241 CAAGCAATTAATTAAGAGGTTCCAGTCAATGAAGTGGGCTCCAGTATTAATGAA 3300
QY 3301 TAGGTTCCAGTATGAAACATTCAGAGCAAGCTAGTAGAAACAGAGGCGCAAAATGGA 3360
DB 3301 TAGGTTCCAGTATGAAACATTCAGAGCAAGCTAGTAGAAACAGAGGCGCAAAATGGA 3360
QY 3361 ATGCTATGCTTAAGTAAAGGTTTGAACCTGAGGTTATTAAGAAAGTCTTCTGGA 3420
DB 3361 ATGCTATGCTTAAGTAAAGGTTTGAACCTGAGGTTATTAAGAAAGTCTTCTGGA 3420
QY 3421 GTTAATTTAGCATCTGAAATTAAGAAAGCAAGATTAAGAAAGTGTGAGTCACTGTA 3480
DB 3421 GTTAATTTAGCATCTGAAATTAAGAAAGCAAGATTAAGAAAGTGTGAGTCACTGTA 3480
QY 3481 ATACAGATTTCTTCCATATCTGATTTAGATTAAGAAACAGCTATGGAAGTATGTC 3540

3481 ATACGATTTCTCCATATCTGATTTGAGATTAAGAACAGCTATGGAGATGTC 3540
QY 3541 ATGATCTCAGGTTTGTCTGAGACCTGATGACTGTTATATATGTTGAAATTAAG 3600
Db 3541 ATGATCTCAGGTTTGTCTGAGACCTGATGACTGTTATATATGTTGAAATTAAG 3600
QY 3601 AAGATCTAGTTTGTCTGAAATTAAGATTAAGAAAGTTCTGTTTGTAGCAAAAGCG 3660
Db 3601 AAGATCTAGTTTGTCTGAAATTAAGATTAAGAAAGTTCTGTTTGTAGCAAAAGCG 3660
QY 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCATACATTGGCTCAG 3720
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCATACATTGGCTCAG 3720
QY 3721 GTTACCGAGAGAGGCGCAAAATTAAGAGTCTCTGAGAGAGAACTTATCTATGAGAGT 3780
Db 3721 GTTACCGAGAGAGGCGCAAAATTAAGAGTCTCTGAGAGAGAACTTATCTATGAGAGT 3780
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAACAATATACCTTCTCAGT 3840
QY 3841 CTACTAGGATAGCACCCTGCTACCGAGTGTCTGTTAAGAACACAGAGAGAAATTAAT 3900
Db 3841 CTACTAGGATAGCACCCTGCTACCGAGTGTCTGTTAAGAACACAGAGAGAAATTAAT 3900
QY 3901 TATCATTTGAAGAATAGCTTAATAGTCTGAGTAACAGGATATATTGGCAAGGATCTC 3960
Db 3901 TATCATTTGAAGAATAGCTTAATAGTCTGAGTAACAGGATATATTGGCAAGGATCTC 3960
QY 3961 AGGAACATCACCTTAGTAGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
Db 3961 AGGAACATCACCTTAGTAGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
QY 4021 GTGATTTGGAAGACTTGAAGTCAATTAACAACCCAGAGTCTTTCTTGAATGTTCTT 4080
Db 4021 GTGATTTGGAAGACTTGAAGTCAATTAACAACCCAGAGTCTTTCTTGAATGTTCTT 4080
QY 4081 CCAAAACAAATAGAGGATCAGTGTGAAGCAGAGGAGTGTGCTGAGTGAAGAAATGG 4140
Db 4081 CCAAAACAAATAGAGGATCAGTGTGAAGCAGAGGAGTGTGCTGAGTGAAGAAATGG 4140
QY 4141 TTTGAGATGATGAAGAAAGAGAGACGGCTTGGAGAAATTAATCAAGAGAGCAAGCA 4200
Db 4141 TTTGAGATGATGAAGAAAGAGAGACGGCTTGGAGAAATTAATCAAGAGAGCAAGCA 4200
QY 4201 TGGATTTCAAATCTAGTGAAGCAGATCTGGGTGTGAGAGTGAACAAAGCTCTGAG 4260
Db 4201 TGGATTTCAAATCTAGTGAAGCAGATCTGGGTGTGAGAGTGAACAAAGCTCTGAG 4260
QY 4261 ACTGCTCAGGGCTATCTCTGAGATGACATTTTAACCACTGAGAGAGGATTAACATGC 4320
Db 4261 ACTGCTCAGGGCTATCTCTGAGATGACATTTTAACCACTGAGAGAGGATTAACATGC 4320
QY 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTGTTAGAAACAGC 4380
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTGTTAGAAACAGC 4380
QY 4381 ATGGAGCAGGCTTCTTAACAGCTACCTTCAATAGTACCTCTGCTTGAAG 4440
Db 4381 ATGGAGCAGGCTTCTTAACAGCTACCTTCAATAGTACCTCTGCTTGAAG 4440
QY 4441 ACCGCGCAATCCAGAACAAAGCAGATCAGAAAGAGATTAATCTTACAGAAAGTA 4500
Db 4441 ACCGCGCAATCCAGAACAAAGCAGATCAGAAAGAGATTAATCTTACAGAAAGTA 4500
QY 4501 GTGAATACCTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAGTTTGAAGTCTG 4560
Db 4501 GTGAATACCTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAGTTTGAAGTCTG 4560
QY 4561 CAGATAGTTTACCGTAAATTAAGAAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620
Db 4561 CAGATAGTTTACCGTAAATTAAGAAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620

QY 4621 GCCATCATTTAGATGATAGGTTGATACATGACAGTGTCTGGAGTCTTCAGATAGAA 4680
Db 4621 GCCATCATTTAGATGATAGGTTGATACATGACAGTGTCTGGAGTCTTCAGATAGAA 4680
QY 4681 ACTACCCATCTCAAGAGAGGCTCATTAAGTTGTTGATGAGAGACCAAGCTGAG 4740
Db 4681 ACTACCCATCTCAAGAGAGGCTCATTAAGTTGTTGATGAGAGACCAAGCTGAG 4740
QY 4741 AGTCTGGGCTCACAGATTTGACGGAACATTTACTTGGCAAGGACAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCTCACAGATTTGACGGAACATTTACTTGGCAAGGACAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAATTCGGAATTCAGCTCTCTGATGAGCCCTGAATCTGATCTCTG 4860
Db 4801 CCCCTTACCTGGAATTCGGAATTCAGCTCTCTGATGAGCCCTGAATCTGATCTCTG 4860
QY 4861 AAGACAGAGCCCAAGAGTCAAGCTGCTGTTGGCAACATACCATCTTCAACCTGATGA 4920
Db 4861 AAGACAGAGCCCAAGAGTCAAGCTGCTGTTGGCAACATACCATCTTCAACCTGATGA 4920
QY 4921 AAGTTCCCATTTGAAGTTGACAGAAATCTGCCAGGCTCCAGCTGCTGCTCATATCTG 4980
Db 4921 AAGTTCCCATTTGAAGTTGACAGAAATCTGCCAGGCTCCAGCTGCTGCTCATATCTG 4980
QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGAACAGAGAGAGAACCCAGAAATGACAG 5040
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGAACAGAGAGAGAACCCAGAAATGACAG 5040
QY 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCATGATGTTGTTGCTGCTGACCCCAAG 5100
Db 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCATGATGTTGTTGCTGCTGACCCCAAG 5100
QY 5101 AATTATGCTGCTGATCAAGTTTCCAGAAACCAACATCACTTAACTTAATTA 5160
Db 5101 AATTATGCTGCTGATCAAGTTTCCAGAAACCAACATCACTTAACTTAATTA 5160
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTTGTTGAACGAGAC 5220
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGAGTTGTTGTTGAACGAGAC 5220
QY 5221 TGAATATTTTCTAGAAATTCGGGAGAGAAATGGTAGTTAGTATTTCTGGGTGACC 5280
Db 5221 TGAATATTTTCTAGAAATTCGGGAGAGAAATGGTAGTTAGTATTTCTGGGTGACC 5280
QY 5281 AGCTATTTAAAGAAAGAAATTCGTAATGACATGATTTTGAAGTACAGAGATGTGG 5340
Db 5281 AGCTATTTAAAGAAAGAAATTCGTAATGACATGATTTTGAAGTACAGAGATGTGG 5340
QY 5341 TCAATGGAAGAAACCAACAGGCTCAAGAGGACAGAGAAATCCAGAGACAGAAAGCT 5400
Db 5341 TCAATGGAAGAAACCAACAGGCTCAAGAGGACAGAGAAATCCAGAGACAGAAAGCT 5400
QY 5401 TCAGGGGCTAGAAATCTGTTGCTAGTGGCCCTTACCAACATGCCCCAGATCACTGG 5460
Db 5401 TCAGGGGCTAGAAATCTGTTGCTAGTGGCCCTTACCAACATGCCCCAGATCACTGG 5460
QY 5461 AATGATGCTACAGCTGTGAGTCTCTGAGTGAAGAGCTTATCAATTAACCTTGG 5520
Db 5461 AATGATGCTACAGCTGTGAGTCTCTGAGTGAAGAGCTTATCAATTAACCTTGG 5520
QY 5521 GCACAGGTGTCACCAATTTGTTGTTGAGCAGATGCTGAGACAGAGACAAATGCT 5580
Db 5521 GCACAGGTGTCACCAATTTGTTGTTGAGCAGATGCTGAGACAGAGACAAATGCT 5580
QY 5581 TCATATGCAATTTGGCAGATGTGAGGACCTGTGTGACCCAGAGTGGGTGGACA 5640
Db 5581 TCATATGCAATTTGGCAGATGTGAGGACCTGTGTGACCCAGAGTGGGTGGACA 5640
QY 5641 GTGTAGCACTCTACAGATGCGAGAGCTGACACCTTACCTGATACCCAGATCCCCACA 5700
Db 5641 GTGTAGCACTCTTACAGATGCGAGAGCTGACACCTTACCTGATACCCAGATCCCCACA 5700

QY 5701 GCCACTACTGA 5711
 DB 5701 GCCACTACTGA 5711

RESULT 2
 AAV62180
 ID AAV62180 standard; DNA; 5711 BP.

AAV62180;

11-FEB-1999 (first entry)

BRCA1 (omil) coding sequence.

BRCA1: mutation detection; disease screening; multiple allele variation;
 breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;
 Duchenne muscular dystrophy; Becker muscular dystrophy; ss.

Homo sapiens.

Key Location/Qualifiers
 CDS 120..5711
 FT /tag= a

W09844157-A2.

08-OCT-1998.

26-MAR-1998; 98WO-US06002.

28-MAR-1997; 97US-0825487.

(ONCO-) ONCOMED INC.

Murphy PD, White MB;

WPI; 1998-542713/46.

P-PSDB; AAW79665.

Identifying variations in polynucleotide sequences - using allele
 specific hybridisation assay, sequence variation locating assay, and
 direct sequencing, in a stepwise procedure

Disclosure; Fig 1a-j; 62pp; English.

This sequence encodes the human BRCA (omil) protein, and was used to test
 the method of the invention. The method is for determining the presence
 or absence of a sequence variation in a gene sample, and comprises:
 (a) performing an allele specific hybridisation assay for one or more
 pre-determined sequence variations; (b) if no pre-determined sequence
 variation found in step (a) then performing a sequence variation location
 assay; (c) if no sequence variation found in step (b) then sequencing
 the gene sample; (c1) if sequence variation is found in step (b) then
 targeted confirmatory sequencing is performed; and (d) determining the
 presence of a sequence variation by analysing the sequence(s) obtained in
 step (c) or step (c1) against a reference sample. Alternatively, step
 (a) or step (b) is omitted from the method. The invention provides a
 stepwise and integrated method for the efficient and accurate detection
 of variations in polynucleotide sequences, being directed towards
 screening for diseases associated with multiple allele variations,
 including breast and ovarian cancer, cystic fibrosis, Duchenne and Becker
 muscular dystrophy, and Li-Fraumeni syndrome.

Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;

Query Match 100.0%; Score 5711; DB 19; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTGCTAGAGCTTCTCTGAGACCCGACACAGAGCTGTGGGTTTCTCAATTAAGTGGCC 60
 DB 1 AAGCTGCTAGAGCTTCTCTGAGACCCGACACAGAGCTGTGGGTTTCTCAATTAAGTGGCC 60

QY 61 CCTGCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCATTTGAAACAGAAAGAAA 120
 DB 61 CCTGCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCATTTGAAACAGAAAGAAA 120

QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTACAAATATCTATTAATGCTATGACAGAAA 180
 DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTACAAATATCTATTAATGCTATGACAGAAA 180

QY 181 TCTTAGAGTTCGCCATCTGCTGGAGTTGATCAAGAACTCTCCCAAGAGTGAGAC 240
 DB 181 TCTTAGAGTTCGCCATCTGCTGGAGTTGATCAAGAACTCTCCCAAGAGTGAGAC 240

QY 241 ACATATTTTGGCAATTTTGGCATGCGAAATCTTCAACAGAGAAAGAGGCGCTTCAACAGT 300
 DB 241 ACATATTTTGGCAATTTTGGCATGCGAAATCTTCAACAGAGAAAGAGGCGCTTCAACAGT 300

QY 301 GTCTTTATGTGAAGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360
 DB 301 GTCTTTATGTGAAGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360

QY 361 AACTTGTGAAGAGCTATGAAAAATCATTTGCTTTTCAAGTTCACAGCTTGGAGT 420
 DB 361 AACTTGTGAAGAGCTATGAAAAATCATTTGCTTTTCAAGTTCACAGCTTGGAGT 420

QY 421 ATGCAACAGCTATTAATTTTGGCAAAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480
 DB 421 ATGCAACAGCTATTAATTTTGGCAAAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGATGAGGCTTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 540
 DB 481 AAGTTTCTATCATCCAAAGATGAGGCTTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 540

QY 541 AACCCGAAATTCCTTCTCTGAGGAAACAGCTCAGTCCAACTCTCACTTGA 600
 DB 541 AACCCGAAATTCCTTCTCTGAGGAAACAGCTCAGTCCAACTCTCACTTGA 600

QY 601 CTGTGAGAACTCTGAGACCAAAAGCAGGATTCACACTCAAAAGAGCTCTGCTCATTTG 660
 DB 601 CTGTGAGAACTCTGAGACCAAAAGCAGGATTCACACTCAAAAGAGCTCTGCTCATTTG 660

QY 661 AATTGGAGTCTGATTTCTTGAAGATACGTTAATAGGCAACTTATTGACGTGGAG 720
 DB 661 AATTGGAGTCTGATTTCTTGAAGATACGTTAATAGGCAACTTATTGACGTGGAG 720

QY 721 ATCAAGATTTGTAAATTAATCAACCTCTCAAGAAACAGGATGAAATCAATTTGATTTCTG 780
 DB 721 ATCAAGATTTGTAAATTAATCAACCTCTCAAGAAACAGGATGAAATCAATTTGATTTCTG 780

QY 781 CAAAAAGAGCTGCTGTGAATTTTCTGAGAGGATGTAAACAAATCTGAACATCATCAAC 840
 DB 781 CAAAAAGAGCTGCTGTGAATTTTCTGAGAGGATGTAAACAAATCTGAACATCATCAAC 840

QY 841 CCAGTAATTAATGATTTTGAACCACTGGAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900
 DB 841 CCAGTAATTAATGATTTTGAACCACTGGAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900

QY 901 ATCAGGATGATTTCTTCAAACTTGCATGTGAGACCATGTGGCAAAATCTCATGCA 960
 DB 901 ATCAGGATGATTTCTTCAAACTTGCATGTGAGACCATGTGGCAAAATCTCATGCA 960

QY 961 GCTCATTCACAGATGAGAAACAGCACTTTATTAATCACTTAAGACGAATGATGAGAAA 1020
 DB 961 GCTCATTCACAGATGAGAAACAGCACTTTATTAATCACTTAAGACGAATGATGAGAAA 1020

QY 1021 AAGCTGAATTTCTGTAATTAATTAAGCAAAAGAGGCTTGAAGAGGCAATTAACAGAT 1080
 DB 1021 AAGCTGAATTTCTGTAATTAATTAAGCAAAAGAGGCTTGAAGAGGCAATTAACAGAT 1080

QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGGCGAGCTCCAGACACAGAAAAAGGTAG 1140
 DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGGCGAGCTCCAGACACAGAAAAAGGTAG 1140

1141 ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAAGAAATGGAATAGCAGAAAATGTCATGCT 1200
1141 ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAAGAAATGGAATAGCAGAAAATGTCATGCT 1200
1201 CAGAGAAATCTAGAGATACGTAAGATGTTCTTGGATTAACACTTAATATGACACATTCAGA 1260
1201 CAGAGAAATCTAGAGATACGTAAGATGTTCTTGGATTAACACTTAATATGACACATTCAGA 1260
1261 AAGTAAATGAGTGGTCTTCCAGAAATGAGTGAACCTTTGGTCTGATGATGATGATGATG 1320
1261 AAGTAAATGAGTGGTCTTCCAGAAATGAGTGAACCTTTGGTCTGATGATGATGATGATG 1320
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATGATGATGATGATGATGATGATG 1380
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATGATGATGATGATGATGATGATG 1380
1381 AATATCTGCTTCTTCCAGAGAAATAGACTTAATGAGCAGTATGATGATGATGATGATG 1440
1381 AATATCTGCTTCTTCCAGAGAAATAGACTTAATGAGCAGTATGATGATGATGATGATG 1440
1441 TATGTAAGAGTGAAGAGTTCATGCAAAATGAGTGAATGATGATGATGATGATGATGAT 1500
1441 TATGTAAGAGTGAAGAGTTCATGCAAAATGAGTGAATGATGATGATGATGATGATGAT 1500
1501 TTGGGAAAACCTATGCAAGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
1501 TTGGGAAAACCTATGCAAGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
1561 TAAATTAATGAGAGCATTGTTACTGAGCCACAGATATATACAGAGGAGGAGGAGGAGG 1620
1561 TAAATTAATGAGAGCATTGTTACTGAGCCACAGATATATACAGAGGAGGAGGAGGAGG 1620
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1621 AATTAAGAGTGAAGAGTTCATGCAAAATGAGTGAATGATGATGATGATGATGATGATG 1680
1681 CAGATTTGGCAGTTCAGAAAAGACTCTGAAATGATTAATCAGGGAATTAACCAAGAGAG 1740
1681 CAGATTTGGCAGTTCAGAAAAGACTCTGAAATGATTAATCAGGGAATTAACCAAGAGAG 1740
1741 AGAATGGTCAAGTGAATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800
1741 AGAATGGTCAAGTGAATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800
1801 CTAATTCAGATGAGAAAATCTTAACCCAAATGAAATCACTCGAAAAGAAATCTGCTTTCA 1860
1801 CTAATTCAGATGAGAAAATCTTAACCCAAATGAAATCACTCGAAAAGAAATCTGCTTTCA 1860
1861 AAACGAAAGCTGAACCTTAAGCAGCAGATTAAGCAATATGGAATGGAATCGAATTAATTC 1920
1861 AAACGAAAGCTGAACCTTAAGCAGCAGATTAAGCAATATGGAATGGAATCGAATTAATTC 1920
1921 ACAATTTCAAAAGCAGCTTAAGAAAGATAGCTGAGAGAGAGAGCTTTCTTACAGAGCATTTTC 1980
1921 ACAATTTCAAAAGCAGCTTAAGAAAGATAGCTGAGAGAGAGAGCTTTCTTACAGAGCATTTTC 1980
1981 ATGGGCTTGAAGCTAGTATGATGATGATTAAGCAATGAGCAGCTTAATGATGATGATGAT 2040
1981 ATGGGCTTGAAGCTAGTATGATGATGATTAAGCAATGAGCAGCTTAATGATGATGATGAT 2040
1981 ATGGGCTTGAAGCTAGTATGATGATGATTAAGCAATGAGCAGCTTAATGATGATGATGAT 2040
2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAGAAAGTAAACCAAAATGAGCAGTCA 2100
2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAGAAAGTAAACCAAAATGAGCAGTCA 2100
2101 GGGCAGAGAGAACTTACAACTCATGAGAGGTAAGAACTGCAACTGAGAGCAAGAGAA 2160
2101 GGGCAGAGAGAACTTACAACTCATGAGAGGTAAGAACTGCAACTGAGAGCAAGAGAA 2160
2161 GTAAACAGCCAAATGAGAGAGCAAGTAAAGACATGAGAGTCTTTCCAGAGAGCTGA 2220
2161 GTAAACAGCCAAATGAGAGAGCAAGTAAAGACATGAGAGTCTTTCCAGAGAGCTGA 2220
2221 AGTTAAACAAATGAGAGCTGCTTCTTTACTAAGTGTTCAAATACAGTGAATTTAAAGAT 2280

2221 AGTTAAACAAATGAGAGCTGCTTCTTTACTAAGTGTTCAAATACAGTGAATTTAAAGAT 2280
2281 TTGTCAATCTTACGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
2281 TTGTCAATCTTACGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
2341 CTAATTAATGCTGAAG 2400
2341 CTAATTAATGCTGAAG 2400
2401 AAAGATCTGAG 2460
2401 AAAGATCTGAG 2460
2461 AAAGATCTGAG 2520
2461 AAAGATCTGAG 2520
2521 GTGTGAGTCAAGTGAAG 2580
2521 GTGTGAGTCAAGTGAAG 2580
2581 AATTAAG 2640
2581 AATTAAG 2640
2641 GGGGAAACAGAGATGAG 2700
2641 GGGGAAACAGAGATGAG 2700
2701 TCAAGGTTTCAAAAG 2760
2701 TCAAGGTTTCAAAAG 2760
2761 AATGTGCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
2761 AATGTGCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820
2821 TTGAATGAG 2880
2821 TTGAATGAG 2880
2881 AGACAGTGAATATATCTGAG 2940
2881 AGACAGTGAATATATCTGAG 2940
2941 ATGCCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000
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3001 ACGAAACCTGAGCTATTAATCTCAATTAAGCAATGAGAGAGAGAGAGAGAGAGAGAGAG 3060
3001 ACGAAACCTGAGCTATTAATCTCAATTAAGCAATGAGAGAGAGAGAGAGAGAGAGAGAG 3060
3061 CACCACTTTTCCATGAG 3120
3061 CACCACTTTTCCATGAG 3120
3121 AAAAATTTGAG 3180
3121 AAAAATTTGAG 3180
3181 GTACAGTGAAG 3240
3181 GTACAGTGAAG 3240
3241 CAAGCAATATTAAG 3300
3241 CAAGCAATATTAAG 3300
3301 TAGGTTCAAGTGAAG 3360

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QY 3361 ATGCTATGCTTAATTAGGGGTTTTGCAACCTGAGGCTATAACAAAGCTTCCTGGAA 3420
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DB 5701 GCCCACTACTGA 5711

RESULT 3

AAV46448 ID AAV46448 standard; cDNA: 5711 BP.

AAV46448;

18-NOV-1998 (first entry)

Human BRCA1 om1 cDNA.

BRCA1; om1; human; breast and ovarian cancer predisposing gene;
polymorphism; susceptibility; anti-oncogene; tumour suppressor;
chromosome 17q; ss.

Homo sapiens.

Key Location/Qualifiers
FT 120..5711
CDS /*tag= a
/product= "BRCA1 om1 protein"

US5750400-A.

12-MAY-1998.

12-FEB-1997; 97US-0798691.

12-FEB-1996; 96US-0598591.

12-FEB-1997; 97US-0798691.

(ONCO-) ONCOMED INC.

Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,

Schelter DB, Zeng B;

WPI, 1998-296774/26.

P-PSDB; AAW76098.

BRCA1 om1 gene coding sequences - useful for distinguishing between

polymorphisms and mutation(s) in the screening for disposition to

breast or ovarian cancer

Claim 2d; Column 27-32; 54pp; English.

This sequence encodes the human BRCA1 (breast and ovarian cancer
predisposing gene) om1 gene. This sequence and polymorphic variations of
this sequence are useful for the identification of an individual who may
or may not have an increased susceptibility to breast or ovarian cancer.
The sequences used identify gene changes which are due to polymorphisms,
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
suppressor) which is involved in genetic inheritance of cancers.
Especially breast and ovarian cancer. It is found at human chromosome 17q
which is known to be linked to cancer susceptibility, especially breast
cancer. Cells containing a mutation in this gene lose the wild-type
function of BRCA1 and are more susceptible to cancers.

Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;

Query Match 100.0%; Score 5711; DB 19; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCTTCGAGACATTCCTGACACCCGACAGAGCTGTGGGTTCTCAGATACTGGGCC 60
QY 61 CCTGCGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAGTTCAATGGAACAGAGAAA 120
DB 61 CCTGCGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAGTTCAATGGAACAGAGAAA 120
QY 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTAAATGCTAATGATGAGAGAAA 180
DB 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTAAATGCTAATGATGAGAGAAA 180
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DB 841 CCAGTAATTAATGATTTGAACCACTGAGAGGCTGAGGCTGAGAGGCTTCCAGAAAGT 900
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DB 5701 GCCACTACTGA 5711

RESULT 5
AAV46470
ID AAV46470 standard; cDNA, 5711 BP.
XX
AC AAV46470;
XX
DT 18-NOV-1998 (first entry)
XX
DE Human BRCA1 omi3 polymorphism #6 cDNA.
XX
KM BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KM polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KM chromosome 17q; ss.
XX
OS Homo sapiens.
XX
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FT FT /product= "BRCA1 omi3 protein"
FT FT 4427
FT FT /*tag= b
FT FT /note= "This polymorphic variation can be a T or C
nucleotide"
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XX
XX PD 12-MAY-1998.
XX
XX PF 12-FEB-1997; 97US-0798691.
XX
XX PR 12-FEB-1996; 96US-0598591.
XX PR 12-FEB-1997; 97US-0798691.
XX
XX PA (ONCO-) ONCOMED INC.
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XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI Scheller DB, Zeng B;
XX WPI: 1998-296774/26.
DR
XX BRCA1 omi3 gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
XX Claim 2e, Page -: 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
CC nucleotide 4427. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi3 gene represented in AAV46450.
XX
SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB:19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAAAGGCACTTATTCAGTGTGGAG 720
QY 721 ATCAAGAAATTGTACAAATCACCCCTCAAGGAACAGGATGAATCAGTTGGATTCTG 780
DB 721 ATCAAGAAATTGTACAAATCACCCCTCAAGGAACAGGATGAATCAGTTGGATTCTG 780
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAACTCAATCTGAACTATCAAC 840
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAACTCAATCTGAACTATCAAC 840
QY 841 CCGATTAATATGATTTTGAACACCACTGAGAAAGCTGAGTGAAGGCACTCCGAAAGT 900
DB 841 CCGATTAATATGATTTTGAACACCACTGAGAAAGCTGAGTGAAGGCACTCCGAAAGT 900
QY 901 ATCAGGATAGTTCTGTTTCAAACTTGATGTGAGCATGTGACAAATCTCATGCCA 960
DB 901 ATCAGGATAGTTCTGTTTCAAACTTGATGTGAGCATGTGACAAATCTCATGCCA 960
QY 961 GCTCATTAAGCATGAGAACAGCAGTTTATCTCACTAAAGACAGATGATGAGAA 1020
DB 961 GCTCATTAAGCATGAGAACAGCAGTTTATCTCACTAAAGACAGATGATGAGAA 1020
QY 1021 AGGCTGAATTTCTTAATTAAGCAACAGCTGTGCTTACGAGAGGCAATACAGAT 1080
DB 1021 AGGCTGAATTTCTTAATTAAGCAACAGCTGTGCTTACGAGAGGCAATACAGAT 1080
QY 1081 GGGCTGGAAGTGAAGAAACATGTAATGATGAGCGGACCTCCAGACAGAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTGAAGAAACATGTAATGATGAGCGGACCTCCAGACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATGAAATGAGAACTGCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATGAAATGAGAACTGCCATGCT 1200
QY 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGATTAACATTAATAGCAGATTCAAA 1260
DB 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGATTAACATTAATAGCAGATTCAAA 1260
QY 1261 AAGTTATGATGATGTTTTCAGAAAGTATGATGATTTGACGTTCTGAATCTCATGATG 1320
DB 1261 AAGTTATGATGATGTTTTCAGAAAGTATGATGATTTGACGTTCTGAATCTCATGATG 1320
QY 1321 GGGAGTCTGAATCAAAAGCCAAAGTATGATGATTTGACGTTCTGAATCTCATGATG 1380
DB 1321 GGGAGTCTGAATCAAAAGCCAAAGTATGATGATTTGACGTTCTGAATCTCATGATG 1380
QY 1381 AATATTTCTGTTTCTTCAAGAGAAATGACTTACTGCGCAGTGTCTCTAATGAGGCTTTAA 1440
DB 1381 AATATTTCTGTTTCTTCAAGAGAAATGACTTACTGCGCAGTGTCTCTAATGAGGCTTTAA 1440
QY 1441 TATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGTAATTTGAAGCAAAATAT 1500
DB 1441 TATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGTAATTTGAAGCAAAATAT 1500
QY 1501 TTGGAAAACTATCGGAAGAGGCAAGCTCCCACTTAAGCCATGTATCGAAATATC 1560
DB 1501 TTGGAAAACTATCGGAAGAGGCAAGCTCCCACTTAAGCCATGTATCGAAATATC 1560
QY 1561 TAAATTTAGAGATTTGTTTACTGAGCCACAGATATTAAGAAGGCTCCCTCACAATAA 1620
DB 1561 TAAATTTAGAGATTTGTTTACTGAGCCACAGATATTAAGAAGGCTCCCTCACAATAA 1620
QY 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAG 1680
DB 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAG 1680
QY 1681 CAGATTTGCACTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACAAACGAGC 1740

DB 1681 CAGATTTGCACTTCAAAAAGACTCTGAAATATTAATCAGGGAACCTAACAAACGAGC 1740
QY 1741 AGAATGCTCAAGTATGATATTTACTTAATAGTGTATATGAATTAACAAAGGATTT 1800
DB 1741 AGAATGCTCAAGTATGATATTTACTTAATAGTGTATATGAATTAACAAAGGATTT 1800
QY 1801 CTATTGAGATGAGAAAAATCTTAACCCAAATGAATCACTCGAAAAAGATCTGCTTCA 1860
DB 1801 CTATTGAGATGAGAAAAATCTTAACCCAAATGAATCACTCGAAAAAGATCTGCTTCA 1860
QY 1861 AAAAGAACTGAACTTATAGCAGATATGAACTGAACTGAAATTAATATATCC 1920
DB 1861 AAAAGAACTGAACTTATAGCAGATATGAACTGAACTGAAATTAATATATCC 1920
QY 1921 ACAATTCAAAACCTTAAGAAATGAGTGAAGGAAAGTCTTACAGGCAATTC 1980
DB 1921 ACAATTCAAAACCTTAAGAAATGAGTGAAGGAAAGTCTTACAGGCAATTC 1980
QY 1981 ATGCGCTGAATAGTATGATGATGAAATCTTAAGCCCACTAATTTGACTGAATTCGAA 2040
DB 1981 ATGCGCTGAATAGTATGATGATGAAATCTTAAGCCCACTAATTTGACTGAATTCGAA 2040
QY 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAAAGTACCAACCAATGCCAGTCA 2100
DB 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAAAGTACCAACCAATGCCAGTCA 2100
QY 2101 GGCACAGCAAAACCTTAACATCTAGGAAGTGAAGAACTTCACTGAGCCAGAAAGA 2160
DB 2101 GGCACAGCAAAACCTTAACATCTAGGAAGTGAAGAACTTCACTGAGCCAGAAAGA 2160
QY 2161 GTAAACAGCAATGAACAGCAAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220
DB 2161 GTAAACAGCAATGAACAGCAAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220
QY 2221 AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAGAAT 2280
DB 2221 AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAGAAT 2280
QY 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTTAAGAAACGTTAAAGTCT 2340
DB 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTTAAGAAACGTTAAAGTCT 2340
QY 2341 CTAAATATGCTGAACACCCCAAGATCTCATGTAAAGTGAAGAGGTTTTCGAAACG 2400
DB 2341 CTAAATATGCTGAACACCCCAAGATCTCATGTAAAGTGAAGAGGTTTTCGAAACG 2400
QY 2401 AAAAGTCTGTAGAGATGACAGATTTTCACTGTATCTGTATCTGATTAAGCACTCAG 2460
DB 2401 AAAAGTCTGTAGAGATGACAGATTTTCACTGTATCTGTATTAAGCACTCAG 2460
QY 2461 AAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAAAGCAAAACAGAACCAATTAAT 2520
DB 2461 AAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAAAGCAAAACAGAACCAATTAAT 2520
QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580
DB 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCCAAGGACTAATTCATGTTGTTCCAAAG 2580
QY 2581 ATTAATGAAATGACACAGAAAGCTTTAAGTATCAATGGGACATGAAGTTAACACAGTC 2640
DB 2581 ATTAATGAAATGACACAGAAAGCTTTAAGTATCAATGGGACATGAAGTTAACACAGTC 2640
QY 2641 GGGAAACAAAGCTAATAATGGAAGAAAGTGAAGTGAATGCTCAGATTTGCGAAATACAT 2700
DB 2641 GGGAAACAAAGCTAATAATGGAAGAAAGTGAAGTGAATGCTCAGATTTGCGAAATACAT 2700
QY 2701 TCAAGTTTCAAAAGGCGCAGTATTTGCTGTTTCAATCCAGAAATGAGAAAGG 2760
DB 2701 TCAAGTTTCAAAAGGCGCAGTATTTGCTGTTTCAATCCAGAAATGAGAAAGG 2760
QY 2761 AATGTGCAACATTTCTGTCCCACTGTGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820

Db	2761	AATGTGCACAACTTCTCTGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Qy	2821	TTGATGTGAACAAAGAGAAAGAAATCAAGAAAGATGATCTTATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGATGATCTTATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGCAGGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGCAGGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTATGATCAAGAGAGGCTTAGTGGTTTGTCTATCATCTCAGTTCAGAGACA	3000
Db	2941	ATGCCAAATGTATGATCAAGAGAGGCTTAGTGGTTTGTCTATCATCTCAGTTCAGAGACA	3000
Qy	3001	ACGAAACTGAGCTCACTTACTCCAAATTAACATGAGACTTTTACAAACCCTATGTATAC	3060
Db	3001	ACGAAACTGAGCTCACTTACTCCAAATTAACATGAGACTTTTACAAACCCTATGTATAC	3060
Qy	3061	CACCACTTTTCCCATCAAGTCACTTTGTTTAAACTAAATGTAGAAAAATCTGCTAAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCACTTTGTTTAAACTAAATGTAGAAAAATCTGCTAAGG	3120
Qy	3121	AAAACTTGGAGAACATTCATATGTCACTGACGTAAGAGAAATGGGAAATGAGAACATTCGAA	3180
Db	3121	AAAACTTGGAGAACATTCATATGTCACTGACGTAAGAGAAATGGGAAATGAGAACATTCGAA	3180
Qy	3181	GTACAGTAGACCAATTAGCCGTAATTAACAATTAGAGAAAAATGTTTTTAAAGGACCACT	3240
Db	3181	GTACAGTAGACCAATTAGCCGTAATTAACAATTAGAGAAAAATGTTTTTAAAGGACCACT	3240
Qy	3241	CAAGCAATTTATATAGATAGGTCCAGTACTAATAGAGGGCTCCAGTTTATATGAA	3300
Db	3241	CAAGCAATTTATATAGATAGGTCCAGTACTAATAGAGGGCTCCAGTTTATATGAA	3300
Qy	3301	TAGGTTCCAGTATGAAAAATTCATCAAGCAGAACTAGGTAGAAAACAGAGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAAAATTCATCAAGCAGAACTAGGTAGAAAACAGAGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGATTAGGGGTTTGCACCTGAGGCTTATTAACAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGATTAGGGGTTTGCACCTGAGGCTTATTAACAAGTCTTCTGGAA	3420
Qy	3421	GTAATGTAGATCCTGAAATTAAGAAAGCAAAATATGAAAGATGTTCAGCTGTAA	3480
Db	3421	GTAATGTAGATCCTGAAATTAAGAAAGCAAAATATGAAAGATGTTCAGCTGTAA	3480
Qy	3481	ATACAGATTTTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCCTATGSGAAGTATGC	3540
Db	3481	ATACAGATTTTCTCCATATCTGATTTTCAGATTAACCTTAGAACAGCCTATGSGAAGTATGC	3540
Qy	3541	ATGCATCTCAGGTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGTGTAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGTGTAATTAAGG	3600
Qy	3601	AAGATCTAGTTTGTGTAATAATGAATTAAGAAAGTGTGCTGTTTTAGCAAAAGCG	3660
Db	3601	AAGATCTAGTTTGTGTAATAATGAATTAAGAAAGTGTGCTGTTTTAGCAAAAGCG	3660
Qy	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTATCCGAAGAGGGGCGCAAGAAATTGAGATCCCTCAGAAAGAACTTATCTTAGTAGAGATG	3780
Db	3721	GTATCCGAAGAGGGGCGCAAGAAATTGAGATCCCTCAGAAAGAACTTATCTTAGTAGAGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCAAACCTGTATTTTGTAAAGTAACAAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACCTGTATTTTGTAAAGTAACAAATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGACCCGTGTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGACCCGTGTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900

QY	3901	TATCATTTGAGAAATGCTTTAAATGACTGAGTAACACAGTAATATATGGCAAAAGCATCTC	3968
Db	3901	TATCATTTAGAAATATGCTTTAAATGACTGAGTAACACAGTAATATATGGCAAAAGCATCTC	3968
QY	3961	AGGAACATCACCTTGTAGAGGAAACAAATGTTCTGCTAGCTTGTCTTCTTCCACAGTCA	4020
Db	3961	AGGAACATCACCTTGTAGAGGAAACAAATGTTCTGCTAGCTTGTCTTCTTCCACAGTCA	4020
QY	4021	GTGAATTTGAAAGACTTGACTGCAATACAAACCCAGAGTCTTTCTTGAATGGTCTT	4086
Db	4021	GTGAATTTGAAAGACTTGACTGCAATACAAACCCAGAGTCTTTCTTGAATGGTCTT	4086
QY	4081	CCAAACAAATAGGAGTACAGTCTGAAACCCAGGAGTGGGTCTGAGTCAACAGAAATTGG	4140
Db	4081	CCAAACAAATAGGAGTACAGTCTGAAACCCAGGAGTGGGTCTGAGTCAACAGAAATTGG	4140
QY	4141	TTTCAGATGATGAAAGAAAGAGAAACGGGCTTGGAAAGAAATATTCMAAGAGCAACCA	4200
Db	4141	TTTCAGATGATGAAAGAAAGAGAAACGGGCTTGGAAAGAAATATTCMAAGAGCAACCA	4200
QY	4201	TGGAATTCAAACTTGTAGGTAGACGATTTGGGTGTGAGATGGAAACMAAGCCTCTTGAAG	4266
Db	4201	TGGAATTCAAACTTGTAGGTAGACGATTTGGGTGTGAGATGGAAACMAAGCCTCTTGAAG	4266
QY	4261	ACTGCTCAGGGCTATTCCTCTCAGAGTGCATTTTAAACACTCAGCAGAGGATACATGAC	4320
Db	4261	ACTGCTCAGGGCTATTCCTCTCAGAGTGCATTTTAAACACTCAGCAGAGGATACATGAC	4320
QY	4321	AAACATTAACCTGATTAAGGCTCCAGCAGAAATGGCTGAACCTGATTTAGAACACG	4386
Db	4321	AAACATTAACCTGATTAAGGCTCCAGCAGAAATGGCTGAACCTGATTTAGAACACG	4386
QY	4381	ATGGAGGACAGCCTTCTTAAACAGCTACCTTCATATATAGAGCTCCCTGCGCTTGAAG	4440
Db	4381	ATGGAGGACAGCCTTCTTAAACAGCTACCTTCATATATAGAGCTCCCTGCGCTTGAAG	4440
QY	4441	ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTACAGAAAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTACAGAAAAAGTA	4500
QY	4501	GTGAATTAACCTTATTAAGCCAGAAATCCAGAAAGCCTTTCGCTGACAGATTAGAGTGTG	4566
Db	4501	GTGAATTAACCTTATTAAGCCAGAAATCCAGAAAGCCTTTCGCTGACAGATTAGAGTGTG	4566
QY	4561	CAGATAGTTCACACGATAAAAAATAAGAACACAGAGGTGAAGGTCATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCACACGATAAAAAATAAGAACACAGAGGTGAAGGTCATCCCTCTTAAT	4620
QY	4621	GCCCATCATTTAGATGATGTGTGTATCATGCAAGTGTCTTGGGAGTCTTACAGAAATAGAA	4686
Db	4621	GCCCATCATTTAGATGATGTGTGTATCATGCAAGTGTCTTGGGAGTCTTACAGAAATAGAA	4686
QY	4681	ACTACCCATCTCAAGAGGAGCTCAATTAGAGTGTGTGATGTGAGAGAGCAACAGCTGAGAG	4740
Db	4681	ACTACCCATCTCAAGAGGAGCTCAATTAGAGTGTGTGATGTGAGAGAGCAACAGCTGAGAG	4740
QY	4741	AGTCTGGGCAACACGATTTGACGGAAACATCTTACCTTCCAAAGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCAACACGATTTGACGGAAACATCTTACCTTCCAAAGCAAGATCTAGAGGAA	4800
QY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGAGACCTGGAATCTATCTCTTG	4866
Db	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGAGACCTGGAATCTATCTCTTG	4866
QY	4861	AAGACAGAGCCCCAGAGTCAAGCTGTGTGGCAACATACATCTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTGTGTGGCAACATACATCTTCAACCTCTGATTTGA	4920
QY	4921	AAAGTTCCCAATTGAAAGTGTGAGATGTGCCCAAGGCTCAGCTGTCTCTATACTACTG	4986
Db	4921	AAAGTTCCCAATTGAAAGTGTGAGATGTGCCCAAGGCTCAGCTGTCTCTATACTACTG	4986

Chr	Position	Gene	Accession	Length	GC	GC3	GC3+5	GC3-5	GC3-10	GC3-15	GC3-20	GC3-25	GC3-30	GC3-35	GC3-40	GC3-45	GC3-50	GC3-55	GC3-60	GC3-65	GC3-70	GC3-75	GC3-80	GC3-85	GC3-90	GC3-95	GC3-100	GC3-105	GC3-110	GC3-115	GC3-120	GC3-125	GC3-130	GC3-135	GC3-140	GC3-145	GC3-150	GC3-155	GC3-160	GC3-165	GC3-170	GC3-175	GC3-180	GC3-185	GC3-190	GC3-195	GC3-200	GC3-205	GC3-210	GC3-215	GC3-220	GC3-225	GC3-230	GC3-235	GC3-240	GC3-245	GC3-250	GC3-255	GC3-260	GC3-265	GC3-270	GC3-275	GC3-280	GC3-285	GC3-290	GC3-295	GC3-300	GC3-305	GC3-310	GC3-315	GC3-320	GC3-325	GC3-330	GC3-335	GC3-340	GC3-345	GC3-350	GC3-355	GC3-360	GC3-365	GC3-370	GC3-375	GC3-380	GC3-385	GC3-390	GC3-395	GC3-400	GC3-405	GC3-410	GC3-415	GC3-420	GC3-425	GC3-430	GC3-435	GC3-440	GC3-445	GC3-450	GC3-455	GC3-460	GC3-465	GC3-470	GC3-475	GC3-480	GC3-485	GC3-490	GC3-495	GC3-500	GC3-505	GC3-510	GC3-515	GC3-520	GC3-525	GC3-530	GC3-535	GC3-540	GC3-545	GC3-550	GC3-555	GC3-560	GC3-565	GC3-570	GC3-575	GC3-580	GC3-585	GC3-590	GC3-595	GC3-600	GC3-605	GC3-610	GC3-615	GC3-620	GC3-625	GC3-630	GC3-635	GC3-640	GC3-645	GC3-650	GC3-655	GC3-660	GC3-665	GC3-670	GC3-675	GC3-680	GC3-685	GC3-690	GC3-695	GC3-700	GC3-705	GC3-710	GC3-715	GC3-720	GC3-725	GC3-730	GC3-735	GC3-740	GC3-745	GC3-750	GC3-755	GC3-760	GC3-765	GC3-770	GC3-775	GC3-780	GC3-785	GC3-790	GC3-795	GC3-800	GC3-805	GC3-810	GC3-815	GC3-820	GC3-825	GC3-830	GC3-835	GC3-840	GC3-845	GC3-850	GC3-855	GC3-860	GC3-865	GC3-870	GC3-875	GC3-880	GC3-885	GC3-890	GC3-895	GC3-900	GC3-905	GC3-910	GC3-915	GC3-920	GC3-925	GC3-930	GC3-935	GC3-940	GC3-945	GC3-950	GC3-955	GC3-960	GC3-965	GC3-970	GC3-975	GC3-980	GC3-985	GC3-990	GC3-995	GC3-1000	GC3-1005	GC3-1010	GC3-1015	GC3-1020	GC3-1025	GC3-1030	GC3-1035	GC3-1040	GC3-1045	GC3-1050	GC3-1055	GC3-1060	GC3-1065	GC3-1070	GC3-1075	GC3-1080	GC3-1085	GC3-1090	GC3-1095	GC3-1100	GC3-1105	GC3-1110	GC3-1115	GC3-1120	GC3-1125	GC3-1130	GC3-1135	GC3-1140	GC3-1145	GC3-1150	GC3-1155	GC3-1160	GC3-1165	GC3-1170	GC3-1175	GC3-1180	GC3-1185	GC3-1190	GC3-1195	GC3-1200	GC3-1205	GC3-1210	GC3-1215	GC3-1220	GC3-1225	GC3-1230	GC3-1235	GC3-1240	GC3-1245	GC3-1250	GC3-1255	GC3-1260	GC3-1265	GC3-1270	GC3-1275	GC3-1280	GC3-1285	GC3-1290	GC3-1295	GC3-1300	GC3-1305	GC3-1310	GC3-1315	GC3-1320	GC3-1325	GC3-1330	GC3-1335	GC3-1340	GC3-1345	GC3-1350	GC3-1355	GC3-1360	GC3-1365	GC3-1370	GC3-1375	GC3-1380	GC3-1385	GC3-1390	GC3-1395	GC3-1400	GC3-1405	GC3-1410	GC3-1415	GC3-1420	GC3-1425	GC3-1430	GC3-1435	GC3-1440	GC3-1445	GC3-1450	GC3-1455	GC3-1460	GC3-1465	GC3-1470	GC3-1475	GC3-1480	GC3-1485	GC3-1490	GC3-1495	GC3-1500	GC3-1505	GC3-1510	GC3-1515	GC3-1520	GC3-1525	GC3-1530	GC3-1535	GC3-1540	GC3-1545	GC3-1550	GC3-1555	GC3-1560	GC3-1565	GC3-1570	GC3-1575	GC3-1580	GC3-1585	GC3-1590	GC3-1595	GC3-1600	GC3-1605	GC3-1610	GC3-1615	GC3-1620	GC3-1625	GC3-1630	GC3-1635	GC3-1640	GC3-1645	GC3-1650	GC3-1655	GC3-1660	GC3-1665	GC3-1670	GC3-1675	GC3-1680	GC3-1685	GC3-1690	GC3-1695	GC3-1700	GC3-1705	GC3-1710	GC3-1715	GC3-1720	GC3-1725	GC3-1730	GC3-1735	GC3-1740	GC3-1745	GC3-1750	GC3-1755	GC3-1760	GC3-1765	GC3-1770	
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FT	variation	2201	+/tag= b	FT
FT			/note= "This polymorphic variation can be a C or T nucleotide"	FT
US5750400-A.				
12-MAY-1998.				
12-FEB-1997;	97US-0798691.			
12-FEB-1996;	96US-0598591.			
12-FEB-1997;	97US-0798691.			
(ONCO-) ONCORMED INC.				
Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;				
Schelter DB, Zeng B;				
WPI; 1998-2965774/26.				
BRCA1 omi gene coding sequences - useful for distinguishing between polymorphisms and mutation(s) in the screening for disposition to breast or ovarian cancer				
Claim 2e; Page -; 54pp; English.				
This sequence encodes a human BRCA1 (breast and ovarian cancer predisposing gene) omi gene in which a polymorphic variation occurs at nucleotide 2201. This sequence and other polymorphic variations of this sequence are useful for the identification of an individual who may or may not have an increased susceptibility to breast or ovarian cancer. The sequences used identify gene changes which are due to polymorphisms, rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour suppressor) which is involved in genetic inheritance of cancers, especially breast and ovarian cancer. It is found at human chromosome 17q which is known to be linked to cancer susceptibility, especially breast cancer. Cells containing a mutation in this gene lose the wild-type function of BRCA1 and are more susceptible to cancers. NOTE: This sequence does not appear in the specification but has been created from the wild type BRCA1 omi gene represented in AAIV46448.				
Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1381 T; 1 other;				
Query Match	100.0%;	Score 5710.6;	DB 19;	Length 5711;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5710;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
1 AGCTGCGTGAAGCTTCTGTGAGCCCGGACGAGCTGTGGGGTTTCTGAGTAAGTGGCC	60			
1 AGCTGCGTGAAGCTTCTGTGAGCCCGGACGAGCTGTGGGGTTTCTGAGTAAGTGGCC	60			
61 CTGCGCTCAGGAGGCTTCAACCTCTGCTGTGGGTAAAGTTCAATGGACAGAAAGAA	120			
61 CTGCGCTCAGGAGGCTTCAACCTCTGCTGTGGGTAAAGTTCAATGGACAGAAAGAA	120			
121 TGGATTATATCGCTCTTGGGTTGAAAGATGACAAATGTCATTAATGCTATGGAGAAA	180			
121 TGGATTATATCGCTCTTGGGTTGAAAGATGACAAATGTCATTAATGCTATGGAGAAA	180			
181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGGAACCTGTCTCCACAAGGTGACC	240			
181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGGAACCTGTCTCCACAAGGTGACC	240			
241 ACATATTTTGGCAATTTTGCATGTGAAACTTCTCAACGAGAGAAAGGCTTCAAGT	300			
241 ACATATTTTGGCAATTTTGCATGTGAAACTTCTCAACGAGAGAAAGGCTTCAAGT	300			
301 GTCTTATATGTAAGATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC	360			
301 GTCTTATATGTAAGATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC	360			
361 AACTGTGTGAAGACTATTTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGAGT	420			

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Db 361 AACTGTTGAAGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGACACAGGTTGAGAT 420
Qy 421 ATGCAAAAGCTATTAATTTTGCAGAAAAGAAAATTAATCTCTCTGAAACATCTTAAAGATG 480
Db 421 ATGCAAAAGCTATTAATTTTGCAGAAAAGAAAATTAATCTCTCTGAAACATCTTAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGGCCAAAAGACTTTTACAGAGT 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGGCCAAAAGACTTTTACAGAGT 540
Qy 541 AACCAGAAAATCTCTCTGAGAAAACAGCTCAGTCTCAACTCTTAACTTTGAA 600
Db 541 AACCAGAAAATCTCTCTGAGAAAACAGCTCAGTCTCAACTCTTAACTTTGAA 600
Qy 601 CTGTGAGAACTCTGAGAACAAAGCAGCGGATCAACTCAAAAGAGCTGTCTACATTTG 660
Db 601 CTGTGAGAACTCTGAGAACAAAGCAGCGGATCAACTCAAAAGAGCTGTCTACATTTG 660
Qy 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATPAAGCACTTATTCAGTGGGAG 720
Db 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATPAAGCACTTATTCAGTGGGAG 720
Qy 721 ATCAAGAATGTTTACAAATCAACCCCTCAAGAAACAGGATGAAATCAGTTTGAATTCG 780
Db 721 ATCAAGAATGTTTACAAATCAACCCCTCAAGAAACAGGATGAAATCAGTTTGAATTCG 780
Qy 781 CAAAAAGAGCTGCTGTGTAATTTTCTGAGACGAGTGTAAACAATACTGAAACATCATCAAC 840
Db 781 CAAAAAGAGCTGCTGTGTAATTTTCTGAGACGAGTGTAAACAATACTGAAACATCATCAAC 840
Qy 841 CCAGTAATATATGATTTGAAACACCTGAGAACGCTGAGAGGCACTTCCAGAAAAT 900
Db 841 CCAGTAATATATGATTTGAAACACCTGAGAACGCTGAGAGGCACTTCCAGAAAAT 900
Qy 901 ATCAGGATGATCTGTTTCAAACTTGACATGTGAGCCATGTGGCAAAATCTCAGTCCA 960
Db 901 ATCAGGATGATCTGTTTCAAACTTGACATGTGAGCCATGTGGCAAAATCTCAGTCCA 960
Qy 961 GCTCATTAACAGATGAGAACAGCAGTTTATTACTCACTAAGACAGATGAAATGTGAAA 1020
Db 961 GCTCATTAACAGATGAGAACAGCAGTTTATTACTCACTAAGACAGATGAAATGTGAAA 1020
Qy 1021 AAGCTGAATCTGTAATAAAGCAACAGCTGGCTGTACAGAGAGCCAACTTAACAGAT 1080
Db 1021 AAGCTGAATCTGTAATAAAGCAACAGCTGGCTGTACAGAGAGCCAACTTAACAGAT 1080
Qy 1081 GGGCTGGAAGTAAGAAACATGTAAATGATAGCGGACTCCACAGCAGAAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTAAGAAACATGTAAATGATAGCGGACTCCACAGCAGAAAAAAGGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAAATTAAGCAGAAAATCTGCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAAATTAAGCAGAAAATCTGCATGCT 1200
Qy 1201 CAGAGAACTCTAGAGATCTGAAGATGCTTGTGATAACATTAATTAACAGATTCAGA 1260
Db 1201 CAGAGAACTCTAGAGATCTGAAGATGCTTGTGATAACATTAATTAACAGATTCAGA 1260
Qy 1261 AAGTTAATGAGTGTCTTCCAGAGATGAACTGTGATGTTCTGATGACTCAGATGATG 1320
Db 1261 AAGTTAATGAGTGTCTTCCAGAGATGAACTGTGATGTTCTGATGACTCAGATGATG 1320
Qy 1321 GGGAGCTCTGAATCAAAATGCAAAAGTATGATGATGAGCTTCTTAAATGAGATGATG 1380
Db 1321 GGGAGCTCTGAATCAAAATGCAAAAGTATGATGATGAGCTTCTTAAATGAGATGATG 1380
Qy 1381 AATATTTGAGTCTTCTCAGAGAAAATGACTTAATGAGGAGTCTCTCATGAGCTTTAA 1440
Db 1381 AATATTTGAGTCTTCTCAGAGAAAATGACTTAATGAGGAGTCTCTCATGAGCTTTAA 1440
Qy 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATATATTTGAAGACAAATAT 1500
Db 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATATATTTGAAGACAAATAT 1500

Db 1501 TTGGGAAAACCTATATGGAAGAGGACGCTCCCACTTAAGCATATGTAATCAAAATC 1560
Qy 1501 TTGGGAAAACCTATATGGAAGAGGACGCTCCCACTTAAGCATATGTAATCAAAATC 1560
Db 1561 TTAATATGAGAGACTTTGTTACTGAGCAGACAGATATCAAGAGCGTCCCTCAATA 1620
Qy 1561 TTAATATGAGAGACTTTGTTACTGAGCAGACAGATATCAAGAGCGTCCCTCAATA 1620
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Qy 1621 AATTAAGCGTAAAGAGAGACCTTACATCAGGCTTTCCTGAGGATTTTATCAAGAAAG 1680
Db 1681 CAGATTTGGCAGTTTCAAAAGACTCTGAAATGATTAATCAGGGAACCTAACAAAGGAGC 1740
Qy 1681 CAGATTTGGCAGTTTCAAAAGACTCTGAAATGATTAATCAGGGAACCTAACAAAGGAGC 1740
Db 1741 AGAATGCTCAAGTGTGAATATTTACTAATAGTGTCTATGAGATTAATAAGAGTAT 1800
Qy 1741 AGAATGCTCAAGTGTGAATATTTACTAATAGTGTCTATGAGATTAATAAGAGTAT 1800
Db 1801 CTATTCAGATGAGAAAAATCTTAACCCATAGATCACTGAAAAAGATCTGCTTTCA 1860
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCCATAGATCACTGAAAAAGATCTGCTTTCA 1860
Db 1861 AAGCAAAAGCTGAACCTTAATAGCAGCATATTAACCAATATGGAATCTGAATTAATATCC 1920
Qy 1861 AAGCAAAAGCTGAACCTTAATAGCAGCATATTAACCAATATGGAATCTGAATTAATATCC 1920
Db 1921 ACAAATTCAAAAGACCTTAATAAGATAGGCTGAGAGGAAAGTCTTCTACAGAGCATATTC 1980
Qy 1921 ACAAATTCAAAAGACCTTAATAAGATAGGCTGAGAGGAAAGTCTTCTACAGAGCATATTC 1980
Db 1981 ATGCGCTTGAACCTAGTACTAGTAAATCTTAAGCCCACTTAATTTGATCTGAATTCGAA 2040
Qy 1981 ATGCGCTTGAACCTAGTACTAGTAAATCTTAAGCCCACTTAATTTGATCTGAATTCGAA 2040
Db 2041 TTGATAGTGTCTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAATATGCACTCA 2100
Qy 2041 TTGATAGTGTCTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAATATGCACTCA 2100
Db 2101 GGCACAGCAGAAACCTTAACATCTCATGTGAAGTAAAGAACTGCACTGAGCCAAAGAA 2160
Qy 2101 GGCACAGCAGAAACCTTAACATCTCATGTGAAGTAAAGAACTGCACTGAGCCAAAGAA 2160
Db 2161 GTTACAGCCAAATGACAGACAAATGAATGACATGATGATCTTCCAGAGCTGA 2220
Qy 2161 GTTACAGCCAAATGACAGACAAATGAATGACATGATGATCTTCCAGAGCTGA 2220
Db 2221 AGTTAAACAAATGACACCTGCTTCTTACTAGTGTCAATTAACAGATGAAAT 2280
Qy 2221 AGTTAAACAAATGACACCTGCTTCTTACTAGTGTCAATTAACAGATGAAAT 2280
Db 2281 TTGTCAATCTAGACCTTCCAGAGAGAAAAGAGAAAAGTAAAGT 2340
Qy 2281 TTGTCAATCTAGACCTTCCAGAGAGAAAAGAGAAAAGTAAAGT 2340
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAAGGTTTTCAGAACTG 2400
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAAGGTTTTCAGAACTG 2400
Db 2401 AAAGATCTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2460
Qy 2401 AAAGATCTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2460
Db 2461 AAAGATCTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2520
Qy 2461 AAAGATCTGTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2520
Db 2521 GTGTGAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGACCTAATTCATGTGTTTCCAAAG 2580
Qy 2521 GTGTGAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGACCTAATTCATGTGTTTCCAAAG 2580
Db 2521 GTGTGAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGACCTAATTCATGTGTTTCCAAAG 2580
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OY	2581	ATAATAGAAATGACACACAGAGCTTTAGTATTCATTGGACATGAAGTTACACAGCTC	2640
Db	2581	ATMAATGAAATGACACACAGAGCTTTAGTATTCATTGGACATGAAGTTACACAGCTC	2640
OY	2641	GGGAAACAGCATATGAAATGGAAAGAGTGAATTGATGCTCAGTATTTGGCAATATCAT	2700
Db	2641	GGGAAACAGCATATGAAATGGAAAGAGTGAATTGATGCTCAGTATTTGGCAATATCAT	2700
OY	2701	TCAGAGTTCAAAGGCCAGTCAATTTGGCTGTTTTCAAATCCAGGAAATGCCAAGAGG	2760
Db	2701	TCAGAGTTCAAAGGCCAGTCAATTTGGCTGTTTTCAAATCCAGGAAATGCCAAGAGG	2760
OY	2761	AATGTGCAACATTCCTGCGCCACTCTGGGTCCTTAAGAAACAAAGTCCAAATCTACTT	2820
Db	2761	AATGTGCAACATTCCTGCGCCACTCTGGGTCCTTAAGAAACAAAGTCCAAATCTACTT	2820
OY	2821	TTGAATGTGAACAAAAGGAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
OY	2881	AGACAGTAAATATCATCTGACAGCTTCTGCGTGGTGCACAAAGATTAAGCAGTATATA	2940
Db	2881	AGACAGTAAATATCATCTGACAGCTTCTGCGTGGTGCACAAAGATTAAGCAGTATATA	2940
OY	2941	ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCCAAATGATATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAAGAGCA	3000
OY	3001	ACGAAATCTGACACTATTCTCCAAATAAACATGACATTTTCAAAACCATATGTATAC	3060
Db	3001	ACGAAATCTGACACTATTCTCCAAATAAACATGACATTTTCAAAACCATATGTATAC	3060
OY	3061	CACCACTTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTAAAGAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTAAAGAAATCTGCTAGAGG	3120
OY	3121	AAAACTTTAGAGAACATTCATATGTCACCTGAAAGAGAAATGGAAATGAGAACATTTCAA	3180
Db	3121	AAAACTTTAGAGAACATTCATATGTCACCTGAAAGAGAAATGGAAATGAGAACATTTCAA	3180
OY	3181	GTAACGTAGACAAATTGACCGTAAATACATTAGAGAAATGTTTTAAAGSAGCCAGCT	3240
Db	3181	GTAACGTAGACAAATTGACCGTAAATACATTAGAGAAATGTTTTAAAGSAGCCAGCT	3240
OY	3241	CAAGCAATATTATATGAAGTAGTTCACATATGAATGGAAGTGGGCTCCAGTATTAATGAA	3300
Db	3241	CAAGCAATATTATATGAAGTAGTTCACATATGAATGGAAGTGGGCTCCAGTATTAATGAA	3300
OY	3301	TAGGTTCCAGTATGAAACAACTTCAAGAGAACTTAGTAGAAACAGAGGCCCAAAATTGA	3360
Db	3301	TAGGTTCCAGTATGAAACAACTTCAAGAGAACTTAGTAGAAACAGAGGCCCAAAATTGA	3360
OY	3361	ATGCTATGCTTAGATTAGGGTTTTTGCAACTGAGAGTCTAATAAACAAAGTCTTCTGGA	3420
Db	3361	ATGCTATGCTTAGATTAGGGTTTTTGCAACTGAGAGTCTAATAAACAAAGTCTTCTGGA	3420
OY	3421	GTAATTTGACATCTCTGAAATTAATAAAGCAAGAAATTAAGAAAGTAGTTCAGCTGTA	3480
Db	3421	GTAATTTGACATCTCTGAAATTAATAAAGCAAGAAATTAAGAAAGTAGTTCAGCTGTA	3480
OY	3481	ATTACGATTTCTCCCAATATCTGATTCAGTAACTTAGAACCACCTATGGGAAGTAGTC	3540
Db	3481	ATTACGATTTCTCCCAATATCTGATTCAGTAACTTAGAACCACCTATGGGAAGTAGTC	3540
OY	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGAGATGATGAAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGAGATGATGAAATTAAGG	3600
OY	3601	AAAGATACATGTTTGTCTGAAATTAATGACATTAAGAAAGTTCTGCTGTTTTTAAGCAAAAGCG	3660
Db	3601	AAAGATACATGTTTGTCTGAAATTAATGACATTAAGAAAGTTCTGCTGTTTTTAAGCAAAAGCG	3660

QY	3661	TCGAGAGGAGAGGTTTAGCAGAGAGTCCCTACCCCTTTCACCCATACATTTGGCTCAGG	3720
Db	3661	TCGAGAGGAGAGGTTTAGCAGAGAGTCCCTACCCCTTTCACCCATACATTTGGCTCAGG	3720
QY	3721	GTACCCGAAGAGGGGCCAAGAAATTAGAGTCTTCAGAGAAGAACTTATCTAGTAGAGATG	3780
Db	3721	GTACCCGAAGAGGGGCCAAGAAATTAGAGTCTTCAGAGAAGAACTTATCTAGTAGAGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCACACCTTGTATTTGGTAAAGTAAACATATATCTTCTCACT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACACCTTGTATTTGGTAAAGTAAACATATATCTTCTCACT	3840
QY	3841	CTACTAGGCGATAGACCGGTGGCTACCCAGAGTGTCTGTAAAGAACACAGAGAGAAATTAT	3900
Db	3841	CTACTAGGCGATAGACCGGTGGCTACCCAGAGTGTCTGTAAAGAACACAGAGAGAAATTAT	3900
QY	3901	TATCATTTAAAGATAGCTTAAATGACTGACAGTAAACAGTAATTTGGCAAGGATCTC	3960
Db	3901	TATCATTTAAAGATAGCTTAAATGACTGACAGTAAACAGTAATTTGGCAAGGATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTCTGTAGCTGTCTTCTTCAAGTGCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTCTGTAGCTGTCTTCTTCAAGTGCA	4020
QY	4021	GTGAATTTGGAAAGACTTGACTGCTCAATACAAACACCCAGATCTTCTTGTATTTGGTCTT	4080
Db	4021	GTGAATTTGGAAAGACTTGACTGCTCAATACAAACACCCAGATCTTCTTGTATTTGGTCTT	4080
QY	4081	CCAAACAAATAGGAGCATGCTGTAAAGCCAGGGAGTTGGCTGTAGAGCAAGGAATTGG	4140
Db	4081	CCAAACAAATAGGAGCATGCTGTAAAGCCAGGGAGTTGGCTGTAGAGCAAGGAATTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA	4200
QY	4201	TGGAATTCAAATTTAGGTGAGAGCAGACTCTGGGTTGAGAGTGAACCAAGCTCTTAAG	4260
Db	4201	TGGAATTCAAATTTAGGTGAGAGCAGACTCTGGGTTGAGAGTGAACCAAGCTCTTAAG	4260
QY	4261	ACTGCTCAGGGCTTATCCCTCTCAGAGTACATTTTAACCATCAGACAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTTATCCCTCTCAGAGTACATTTTAACCATCAGACAGAGGATACCATGC	4320
QY	4321	AACATTAACCTGATTAAGGTCCAGCAGAGAAATGGCTGAATCTAGAAGCTGTATTAGAACGC	4380
Db	4321	AACATTAACCTGATTAAGGTCCAGCAGAGAAATGGCTGAATCTAGAAGCTGTATTAGAACGC	4380
QY	4381	ATGGAGCGACGCTTTCTPAACAGCTACCCCTTCATCATTAAGTGACTCCTCTGCTTGAGG	4440
Db	4381	ATGGAGCGACGCTTTCTPAACAGCTACCCCTTCATCATTAAGTGACTCCTCTGCTTGAGG	4440
QY	4441	ACCTGCGAAATCCGAAGCAAAAGCAGTCAAGAAAAGAGATTAATCTTCACAGAAAAGTA	4500
Db	4441	ACCTGCGAAATCCGAAGCAAAAGCAGTCAAGAAAAGAGATTAATCTTCACAGAAAAGTA	4500
QY	4501	GTGAATACCCCTATAGCCAGAAATCCAGAAAGGCTTTTCTGTGCAAGATTGGAGGTCTG	4560
Db	4501	GTGAATACCCCTATAGCCAGAAATCCAGAAAGGCTTTTCTGTGCAAGATTGGAGGTCTG	4560
QY	4561	CAGATAGTCTTACCGATTAATAATTAAGAACCAGAGGTGAAAAGGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTCTTACCGATTAATAATTAAGAACCAGAGGTGAAAAGGTCAATCCCTCTTAAT	4620
QY	4621	GCCCATCATTTAGATGATAGTGTGATCATGACAGTTGCTCTGGGAGCTTTCAGAAATGAA	4680
Db	4621	GCCCATCATTTAGATGATAGTGTGATCATGACAGTTGCTCTGGGAGCTTTCAGAAATGAA	4680
QY	4681	ACTAACCATCTCAAGAGAGGCTCATTTAAGTTTGTGATGTGAGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTAACCATCTCAAGAGAGGCTCATTTAAGTTTGTGATGTGAGAGAGCAACAGCTGGAAG	4740
QY	4741	AGTCTGGGCCACAGATTTGACGAAACATCTTACTTCCAGGCAAGATCTTAGAGGAA	4800

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Db 4741 AGTCTGGGCCACACGATTTGAGGAAACATCTTACTGCGCAAGCAGAACTGATGAGGAA 4800
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Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTTCTCTGATGATACCTGATCTGATCTTCTG 4860
QY 4861 AAGACAGAGCCCAAGTCAGTCGCTGTTGGCAACATCACTTCACTCTGATGATG 4920
Db 4861 AAGACAGAGCCCAAGTCAGTCGCTGTTGGCAACATCACTTCACTCTGATGATG 4920
QY 4921 AAGTTCGCCCAATTGAAAGTTGCAAGATCTGCCAGGGTCAGCTGCTCACTACTACTG 4980
Db 4921 AAGTTCGCCCAATTGAAAGTTGCAAGATCTGCCAGGGTCAGCTGCTCACTACTACTG 4980
QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCGGAGGAAGCAAGATTGACAG 5040
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCGGAGGAAGCAAGATTGACAG 5040
QY 5041 CTTCAACAGAAAGGGTCAACAAAGATGTCATGGTGGTCTGCTGACCCCAAG 5100
Db 5041 CTTCAACAGAAAGGGTCAACAAAGATGTCATGGTGGTCTGCTGACCCCAAG 5100
QY 5101 AATTATGCTCGTGTACAAAGTTGCGAGAAAACACCAATCACTTTAACTTAATTA 5160
Db 5101 AATTATGCTCGTGTACAAAGTTGCGAGAAAACACCAATCACTTTAACTTAATTA 5160
QY 5161 CTGAAGAGACTACTATGTTGTTATGAAAACAGATGCTGATGTTGTGTGAACGAGAC 5220
Db 5161 CTGAAGAGACTACTATGTTGTTATGAAAACAGATGCTGATGTTGTGTGAACGAGAC 5220
QY 5221 TGAATATATTTCTAGAAATGCGGGAGAAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280
Db 5221 TGAATATATTTCTAGAAATGCGGGAGAAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280
QY 5281 AGTCTATTAAAGAAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340
Db 5281 AGTCTATTAAAGAAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340
QY 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAAATCCCGAGACAGAAATCT 5400
Db 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAAATCCCGAGACAGAAATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTTCTATGAGCCCTTCAACAATGCCACAGATCAACTGG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTTCTATGAGCCCTTCAACAATGCCACAGATCAACTGG 5460
QY 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
QY 5521 GCACAGGTGTCACCAATGTCGTTGTCACCAAGTCCCGAGCAAGAAATGCCACAGAT 5580
Db 5521 GCACAGGTGTCACCAATGTCGTTGTCACCAAGTCCCGAGCAAGAAATGCCACAGAT 5580
QY 5581 TCATGCAATTTGGGAGATGTTGAGGACCTGTTGAGACCGAGAGATGGGTGTTGAGA 5640
Db 5581 TCATGCAATTTGGGAGATGTTGAGGACCTGTTGAGACCGAGAGATGGGTGTTGAGA 5640
QY 5641 GTGTAGCACTCTACAGATGTCAGAGAGCTGAGACCTACTGATATCCCAATCCCA 5700
Db 5641 GTGTAGCACTCTACAGATGTCAGAGAGCTGAGACCTACTGATATCCCAATCCCA 5700
QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

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RESULT 7
AAV46452
ID AAV46452 standard; cDNA; 5711 BP.
XX
AC AAV46452;

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XX 18-NOV-1998 (first entry)
DT
XX Human BRCA1 om1 polymorphism #2 cDNA.
DE
XX BRCA1: om1; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KM chromosome 17q; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 120..5711
FT CDS /tag= a
FT /product= "BRCA1 om1 protein"
FT variation 2430
FT /tag= b
FT /note= "This polymorphic variation can be a T or C
FT nucleotide"
XX
XX US5750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-0798691.
XX
XX 12-FEB-1996; 96US-0598591.
XX
XX 12-FEB-1997; 97US-0798691.
XX
XX (ONCO-) ONCORMED INC.
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI Schelter DB, Zeng B;
PI
XX WPI; 1998-296774/26.
XX
XX BRCA1 om1 gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
XX Claim 2e; Page -; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) om1 gene in which a polymorphic variation occurs at
CC nucleotide 2430. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 om1 gene represented in AAV46448.
XX
XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;
SO

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Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGCTGCTGAGACTCTTCTGAGACCCCGACCAAGGCTGTGGGTTCTAGATACTGGGCC 60
Db 1 AGCTGCTGAGACTCTTCTGAGACCCCGACCAAGGCTGTGGGTTCTAGATACTGGGCC 60
QY 61 CTTGGCTCAGAGAGGCTTCACTCTGCTGTGGGTAAGTTCAATTGGAACAGAAAGAAA 120
Db 61 CTTGGCTCAGAGAGGCTTCACTCTGCTGTGGGTAAGTTCAATTGGAACAGAAAGAAA 120
QY 121 TGGATTATCTGCTTCTTGGCGTTGAAGAGTAAGAAATGTCATTATATGTCAGAAAA 180
Db 121 TGGATTATCTGCTTCTTGGCGTTGAAGAGTAAGAAATGTCATTATATGTCAGAAAA 180

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Db 121 TGAATTAATCTGCTCTTCGCGGTGGAAGACATCAAAAATGCTAATTAATGCTATGACAGAAA 180
Qy 181 TCTTAGAGTGTCCATCTGCTGTGAGTTGATCAAGAACTGCTCCACAAGTGTACC 240
Db 181 TCTTAGAGTGTCCATCTGCTGTGAGTTGATCAAGAACTGCTCCACAAGTGTACC 240
Qy 241 ACATATTTTGGCAATTTTGGCATGCTGAACTTCTCAACAGAAAGAGGGCTTTCACAGT 300
Db 241 ACATATTTTGGCAATTTTGGCATGCTGAACTTCTCAACAGAAAGAGGGCTTTCACAGT 300
Qy 301 GTCTTTATATGTAAGAAATGATTAACCAAAAGAGCTTCAAGAAAGTACGATTTAGTC 360
Db 301 GTCTTTATATGTAAGAAATGATTAACCAAAAGAGCTTCAAGAAAGTACGATTTAGTC 360
Qy 361 AACTTGTGAAGAGCTATTTGAAATCATTTTGCTTTTCACTGAGTACAGATTTGGAGT 420
Db 361 AACTTGTGAAGAGCTATTTGAAATCATTTTGCTTTTCACTGAGTACAGATTTGGAGT 420
Qy 421 ATGCAAAACAGCTATTAATTTTGCAGAAAAGGAAATTAATCTCTCTGAAATCTTAAAGATG 480
Db 421 ATGCAAAACAGCTATTAATTTTGCAGAAAAGGAAATTAATCTCTCTGAAATCTTAAAGATG 480
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Db 481 AAGTTTATATCATCAAAAGTATGGGCTTACAGAAACCTGCTCAAAAGATCTTACAGATG 540
Qy 541 AACCGAAATTCCTCTCTGAGAGAAACAGTCTCAGTGTCCAACTCTTACCTTGGAA 600
Db 541 AACCGAAATTCCTCTCTGAGAGAAACAGTCTCAGTGTCCAACTCTTACCTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTCAAAAGACCTGTGTACATTTG 660
Db 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTCAAAAGACCTGTGTACATTTG 660
Qy 661 AATTGGATCTGATCTTCTGGAAGATCCGTTAATTAAGCACTTATGCAAGTGTGGAG 720
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Db	4561	CAGATAGTTCTTACCGATAAAAATAAAGAACCAAGAGTGGAAAGGTCAATCCCTCTCTAAAT	4620
OY	4621	GCCCATCTATTTAGATATAGTGTGTCAATGCCACAGTTGTCTTGGAGTCTTCAGAAATAGAA	4680
Db	4621	GCCCATCTATTTAGATATAGTGTGTCAATGCCACAGTTGTCTTGGAGTCTTCAGAAATAGAA	4680
OY	4681	ACTACCCATCTCAAGAGAGGCTCATTAAGTGTGTGAAGTGGAGAGCAAGCTGGAG	4740
Db	4681	ACTACCCATCTCAAGAGAGGCTCATTAAGTGTGTGAAGTGGAGAGCAAGCTGGAG	4740
OY	4741	AGTCTGGGCCACACAGATTTGACGGAACATCTTACTTCCAAAGGCAAGATCTAAGGGAA	4800
Db	4741	AGTCTGGGCCACACAGATTTGACGGAACATCTTACTTCCAAAGGCAAGATCTAAGGGAA	4800
OY	4801	CCCCCTTACCTGGAAATCTGGAAATCAAGCTCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG	4860
Db	4801	CCCCCTTACCTGGAAATCTGGAAATCAAGCTCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG	4860
OY	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATCCATCTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATCCATCTTCAACCTCTGATTTGA	4920
OY	4921	AAGTTCCCAATTGAAAGTTGCAGATGTGCCAGAGTCCAGCTGTCTCATCTACTG	4980
Db	4921	AAGTTCCCAATTGAAAGTTGCAGATGTGCCAGAGTCCAGCTGTCTCATCTACTG	4980
OY	4981	ATATCTCTGGGTATATATGCAATGGAAGAAAGTGTGAGGAGGAGAGCAAGATTGACAG	5040
Db	4981	ATATCTCTGGGTATATATGCAATGGAAGAAAGTGTGAGGAGGAGAGCAAGATTGACAG	5040
OY	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGGTGTGTCTGAGCCCTGACCCCAAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGGTGTGTCTGAGCCCTGACCCCAAG	5100
OY	5101	AATTTATGCTGTGTACAAAGTTTGGCAGAAAAACAACATCATCTTAACTAATCTAAATTA	5160
Db	5101	AATTTATGCTGTGTACAAAGTTTGGCAGAAAAACAACATCATCTTAACTAATCTAAATTA	5160
OY	5161	CTGAAGAGACTATCTCATGTTGTTATGAAGACAGATGCTGAAGTTGTGTGGAACGACAC	5220
Db	5161	CTGAAGAGACTATCTCATGTTGTTATGAAGACAGATGCTGAAGTTGTGTGGAACGACAC	5220
OY	5221	TGAAATATTTCTAGGAATTCGGGAGGAGAAATGGGTATGATGCTATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTCTAGGAATTCGGGAGGAGAAATGGGTATGATGCTATTTCTGGGTGACCC	5280
OY	5281	AGCTATTTAAAGAAAGAAATAATGCTGATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGCTATTTAAAGAAAGAAATAATGCTGATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
OY	5341	TCATATGGAAGAACCAACCAAGGTCCAAAGCAGACAGAAAGATCCCAAGACAGAAAGATCT	5400
Db	5341	TCATATGGAAGAACCAACCAAGGTCCAAAGCAGACAGAAAGATCCCAAGACAGAAAGATCT	5400
OY	5401	TCAGGGGGCTTGAAGATCTGTGTGCTATGAGGCCCTTCAACCAATGCCCAATCAATCACTGG	5460
Db	5401	TCAGGGGGCTTGAAGATCTGTGTGCTATGAGGCCCTTCAACCAATGCCCAATCAATCACTGG	5460
OY	5461	AATGATATGATCAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCTTCAACCTCTTG	5520
Db	5461	AATGATATGATCAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCTTCAACCTCTTG	5520
OY	5521	GCACAGGTGTACACCCCAATTTGTGTGTGACAGCAGATGCTTGACAGAGGACAATGGCT	5580
Db	5521	GCACAGGTGTACACCCCAATTTGTGTGTGACAGCAGATGCTTGACAGAGGACAATGGCT	5580
OY	5581	TTCAATGCAATTTGGGACAGATGTGTAGAGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
Db	5581	TTCAATGCAATTTGGGACAGATGTGTAGAGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640

QY	5641	GTGTAGACACTCTACGACGTGCAGAGCTGGACACCTACCTGATACCCAGATCCCCACA	5700
Db	5641	GTGTAGACACTCTACGACGTGCAGAGCTGGACACCTACCTGATACCCAGATCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	
RESULT 8			
AAV46453			
AAV46453	standard; cDNA; 5711 BP.		
AAV46453;			
AAV46453;			
18-NOV-1998	(first entry)		
Human BRCA1	om1 polymorphism #3 cDNA.		
BRCA1: om1;	human; breast and ovarian cancer predisposing gene;		
polymorphism;	susceptibility; anti-oncogene; tumour suppressor;		
chromosome 17q; ss.			
Homo sapiens.			
Key	Location/Qualifiers		
CDS	120..5711		
FT	/*tag= a		
FT	/product= "BRCA1 om1 protein"		
FT	2731		
variation	/*tag= b		
FT	/note= "This polymorphic variation can be a C or T		
FT	nucleotide"		
US5750400-A.			
12-MAY-1998.			
12-FEB-1997;	97US-0798691.		
12-FEB-1996;	96US-0598591.		
12-FEB-1997;	97US-0798691.		
(ONCO-) ONCORMED INC.			
Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;			
Schelter DB, Zeng B;			
WPI; 1998-296774/26.			
BRCA1 om1 gene coding sequences - useful for distinguishing between			
polymorphisms and mutation(s) in the screening for disposition to			
breast or ovarian cancer			
Claim 2e; Page -; 54pp; English.			
This sequence encodes a human BRCA1 (breast and ovarian cancer			
predisposing gene) om1 gene in which a polymorphic variation occurs at			
nucleotide 2731. This sequence and other polymorphic variations of this			
sequence are useful for the identification of an individual who may or			
may not have an increased susceptibility to breast or ovarian cancer.			
The sequences used identify gene changes which are due to polymorphisms,			
rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour			
suppressor) which is involved in genetic inheritance of cancers,			
especially breast and ovarian cancer. It is found at human chromosome			
17q which is known to be linked to cancer susceptibility, especially			
breast cancer. Cells containing a mutation in this gene lose the			
wild-type function of BRCA1 and are more susceptible to cancers.			
NOTE: This sequence does not appear in the specification but has been			
created from the wild type BRCA1 om1 gene represented in AAV46448.			
Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1361 T; 1 other;			

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 5710; Conservative 1;

QY 1 AGCTGCTGAGACCTCTGAGACCCCGCACAGGCTGTGGGTTTCTCAGATACTGGGCC 60
DB 1 AGCTGCTGAGACCTCTGAGACCCCGCACAGGCTGTGGGTTTCTCAGATACTGGGCC 60

QY 61 CCTGGCTCAGAGAGCCTTACCCCTCTGCTGGGTTAAAGTTGAAACGAAAGAAA 120
DB 61 CCTGGCTCAGAGAGCCTTACCCCTCTGCTGGGTTAAAGTTGAAACGAAAGAAA 120

QY 121 TGGATTTATCTGCTCTGGCGCTTGAAGAACTCAAAATGTCATTTATGCTATGCAAGAAA 180
DB 121 TGGATTTATCTGCTCTGGCGCTTGAAGAACTCAAAATGTCATTTATGCTATGCAAGAAA 180

QY 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAGAAAGTGACCC 240
DB 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAGAAAGTGACCC 240

QY 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACGAGAAAGAGGCTTACAGT 300
DB 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACGAGAAAGAGGCTTACAGT 300

QY 301 GTCCCTTATGTAAAGATATATACCAAAAGAGCCTACAGAAAGTACAGATTATGTC 360
DB 301 GTCCCTTATGTAAAGATATATACCAAAAGAGCCTACAGAAAGTACAGATTATGTC 360

QY 361 AACTGTGTGAAGAGCTATTTGAAATCATTTGTCTTTGAGCTTGAACAGGTTTGAAT 420
DB 361 AACTGTGTGAAGAGCTATTTGAAATCATTTGTCTTTGAGCTTGAACAGGTTTGAAT 420

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DB 421 ATGCAAAAGCTATATTTTGCAGAAAGAAATTAATCTCTGAAACATCTTAAAGATG 480

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DB 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTCAGTGTCAACTCTTAACTTTGAA 600

QY 601 CTGTGAGAACTCTGAGACAAAGCAGCGATACAACTCAAAAGAGTGTCTACATTTG 660
DB 601 CTGTGAGAACTCTGAGACAAAGCAGCGATACAACTCAAAAGAGTGTCTACATTTG 660

QY 661 AATTGGATCTGATCTTCTGAAAGATACCGTTAATTAAGCACTTAATTCAGTGTGGAG 720
DB 661 AATTGGATCTGATCTTCTGAAAGATACCGTTAATTAAGCACTTAATTCAGTGTGGAG 720

QY 721 ATCAAGAAATGTTTACAATACCCCTCAAGAAACCGAGATGAATCAAGTTGGATTTG 780
DB 721 ATCAAGAAATGTTTACAATACCCCTCAAGAAACCGAGATGAATCAAGTTGGATTTG 780

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QY 841 CCAGTAATTAATGATTTGAACACCACTGAGAACGCTGACAGGCAATCCAGAAAGT 900
DB 841 CCAGTAATTAATGATTTGAACACCACTGAGAACGCTGACAGGCAATCCAGAAAGT 900

QY 901 ATCAGGATGATCTGTTTCAAACTTGATGTGAGAGCATGTGCAAAATACTCATGCA 960
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QY 1081 GGGCTGGAAGTAAGGAAACATGTATATGATGCGGACTCCAGACACAGAAAAAGGTAG 1140
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5701 GCCACTACTGA 5711
5701 GCCACTACTGA 5711

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RESULT 9
AAV46454
ID AAV46454 standard: cDNA, 5711 BP.
XX
XX AAV46454;
AC
XX
XX 18-NOV-1998 (first entry)
DT
XX
DE Human BRCA1 omil polymorphism #4 cDNA.
XX
XX BRCA1, omil; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT FT /*tag= a
FT FT /product= "BRCA1 omil protein"
FT FT variation 3232
FT FT /*tag= b
FT FT /note= "This polymorphic variation can be an A or G
nucleotide"
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XX US750400-A.
XX
XX 12-MAY-1998.
PD
XX
XX 12-FEB-1997; 97US-0798691.
PF
XX
XX 12-FEB-1996; 96US-0598591.
PR
XX 12-FEB-1997; 97US-0798691.
PR
XX
XX (ONCO-) ONCOMED INC.
PA
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI Schelter DB, Zeng B;
PI
XX
XX WPI, 1998-296774/26.
DR
XX
XX BRCA1 omil gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
PS Claim 2e; Page -: 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC

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CC predisposing gene) omi1 gene in which a polymorphic variation occurs at
CC nucleotide 3232. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi1 gene represented in AAV46448.
XX
SQ Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCTCGCTGAGACTTCCTGAGACCCCGACACGAGGTGGGTTTCTCAGATACTGGGCC 60
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DB 121 TGGATTTATGCTGCTTCTGGGTTGAAAGATACAAATGCTATTAATGCTATGCAAGAAA 180
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DB 181 TCTTAAGAGTCCCATCTGCTGAGATGATCAAGAACTCTCTCAACAAAGTGTGACC 240
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DB 601 CTGTGGAACCTGAGAGAACAGCGGATACACCTCAAAAGAGCTGTGTCTACATTTG 660
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DB 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTCAGAGTGGGAG 720
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DB 781 CAAAAAAGGCTGCTGTGAATTTTCTGAGACGAGATGTAACTAATACATCAATCAAC 840
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DB 901 ATCAGGATGATCTGTTTCAAACTTGCATGTGAGAGCAATGAGCAAAATACATGCCA 960
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 QY 4621 GCCCATCATTAAGTGAAGTGTGATCATGACAGTTGCTCTGGAGAGTCTCAGAAATGA 4680
 Db 4621 GCCCATCATTAAGTGAAGTGTGATCATGACAGTTGCTCTGGAGAGTCTCAGAAATGA 4680
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 Db 4681 ACTAACCATTCAAGAGAGAGCTCATTAAGTGTGATGAGAGAGCAACAGCTGGAAG 4740
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 Db 4741 AGTCTGGGCGACAGATTTGACGAAACATCTTAATGCGAAGGCAAGATCTAAGAGGAA 4800
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 Db 4801 CCCCTTACCTGAATCTGAATCAGCCTCTCTGATGACCTGGAATCTGATCTTCTG 4860
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 Db 4921 AAGTCCCAATGAAGTTGAGATTCAGATTCAGAGGCTCCAGGCTGCTGCTCATACATCACTG 4980
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 Db 4981 ATACTCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAGCAAGATTTGACAG 5040
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 Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGCTGAGCTTGAAGCCAGAAAG 5100
 QY 5101 AATTATGCTGTGTCAAGTTTGCAGAAAAACACACATCACTTAATCAATCAATTAATTA 5160
 Db 5101 AATTATGCTGTGTCAAGTTTGCAGAAAAACACACATCACTTAATCAATCAATTAATTA 5160
 QY 5161 CTGAAGAGACTACTCATGTGTGTATGAACACAGATCTGAGTTGTGTGGAACGAGACAC 5220

Db 5161 CTGAAGAGACTACTCATGTGTGTATGAACACAGATCTGAGTTGTGTGGAACGAGACAC 5220
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 Db 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGTACTGATTAATTTCTGGGTACCC 5280
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 Db 5461 AATGATGGAACAGCTGTGTGCTTCTGTGTGAAGAGCTTGCATCAATCACCTTG 5520
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 Db 5521 GCACAGGTGTCCACCAATTTGTGTGTGTCAGCAGCAGATGCTGACAGAGCAATGGCT 5580
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 Db 5641 GTGTAGCACTTACAGAGTCCAGAGCTGGAACCTGATATCCCGAGATCCCCACA 5700
 QY 5701 GCCACTACTGA 5711
 Db 5701 GCCACTACTGA 5711

RESULT 10
 AAV4645
 ID AAV4645 standard; cDNA; 5711 BP.
 XX
 AC AAV4645;
 XX
 DT 18-NOV-1998 (first entry)
 XX
 DE Human BRCA1 om1 polymorphism #5 cDNA.
 XX
 KW BRCA1; om1; human; breast and ovarian cancer predisposing gene;
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 KW chromosome 17q; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 120..5711
 FT FT /*tag= a
 FT /product= "BRCA1 om1 protein"
 FT variation 3667
 FT FT /*tag= b
 FT /note= "This polymorphic variation can be an A or G nucleotide"
 XX
 XX US5750400-A.
 XX PN
 XX PD 12-MAY-1998.
 XX
 XX PF 12-FEB-1997; 97US-0798691.
 XX
 XX PR 12-FEB-1996; 96US-0598591.
 XX
 XX PR 12-FEB-1997; 97US-0798691.

(ONCO-) ONCOMED INC.

PA Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX Scheller DB, Zeng B;
PI WPI, 1998-296774/26.
DR

BRCA1 omi gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer

PS Claim 2e; Page -: 54pp; English.

CC This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi1 gene in which a polymorphic variation occurs at
CC nucleotide 3667. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi1 gene represented in AAV46448.
SQ

Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other:

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTGCGTGAAGACTTCCTGGACCCGCCACAGGCTGTGGGGTTCTCAGATAACTGGGCC 60
DB 1 AGCTGCGTGAAGACTTCCTGGACCCGCCACAGGCTGTGGGGTTCTCAGATAACTGGGCC 60
OY CCTGGCGCTCAGAGAGGCCTTCACTCTGCTCTGGGTAAAGTTCATTGMAACGAAAAGAA 120
DB CCTGGCGCTCAGAGAGGCCTTCACTCTGCTCTGGGTAAAGTTCATTGMAACGAAAAGAA 120
OY 61 CGTGCGCTCAGAGAGGCCTTCACTCTGCTCTGGGTAAAGTTCATTGMAACGAAAAGAA 120
DB 61 CGTGCGCTCAGAGAGGCCTTCACTCTGCTCTGGGTAAAGTTCATTGMAACGAAAAGAA 120
OY 121 TGGATTTATCTGCTCTCTCGCGTTGAAGAAGTCAAAGTCAATTAATGCTATGACAAGAA 180
DB 121 TGGATTTATCTGCTCTCTCGCGTTGAAGAAGTCAAAGTCAATTAATGCTATGACAAGAA 180
OY 121 TGGATTTATCTGCTCTCTCGCGTTGAAGAAGTCAAAGTCAATTAATGCTATGACAAGAA 180
DB 121 TGGATTTATCTGCTCTCTCGCGTTGAAGAAGTCAAAGTCAATTAATGCTATGACAAGAA 180
OY 181 TCTTAGAGTGTCCCATCTGTCTGAGGTGATCAAGGAACCTGTCCCAAGAGTGTACC 240
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGGTGATCAAGGAACCTGTCCCAAGAGTGTACC 240
OY 241 ACATATTTTTGCAAAATTTTGGATGCTGAAACCTTCAACACAGAAAGAGGCCCTTCACAGT 300
DB 241 ACATATTTTTGCAAAATTTTGGATGCTGAAACCTTCAACACAGAAAGAGGCCCTTCACAGT 300
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DB 361 AACCTGTGAAGAGCATTTGAAGAACATTTGTGCTTTTACGTTGACAGAGGTTTGAGT 420
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DB 421 ATGCAAAACAGCTATATTTTGGCAAAAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480
OY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAAGACTTCTACAGAGTG 540
OY 541 AACCCGAAATCTCTTCTTGGCAGAAACCAAGTCTCAGTGTCCAATCTCTTAACCTTGGAA 600
DB 541 AACCCGAAATCTCTTCTTGGCAGAAACCAAGTCTCAGTGTCCAATCTCTTAACCTTGGAA 600

Db	541	TAACCGAAAAATCCCTCTTGTCAGAGAAACCAAGTCTCAGTGTCAACTCTCTAACCTTGAA	600
Qy	601	CTGTGAGAACTCTTGAGGACAAAGCAGGGGATACAACTCCAAAAGACGTCTGTCTACATTG	660
Db	601	CTGTGAGAACTCTAGAGCAAAAGAGGGGATACAACTCAAAAAGACGTCTGTCTACATTG	660
Qy	661	AATTGGGATCGATTCTCTGTAAGATACCGTTAATTAAAGCAACTTATTGCAGTGTGGAG	720
Db	661	AATTGGGATCTGATTCTCTGTAAGATACCGTTAATTAAAGCAACTTATTGCAGTGTGGAG	720
Qy	721	ATCAAGAATTGTTCAAATCAACCCCTCAAGGACCAAGGATGAATCAGTTGGATTCTG	780
Db	721	ATCAAGAATTGTTCAAATCAACCCCTCAAGGACCAAGGATGAATCAGTTGGATTCTG	780
Qy	781	CAAAAAAGCGCTGCTTGTGAATTTTCTGAGAGGATGTACAAATACCTGAACATCATCAAC	840
Db	781	CAAAAAAGCGCTGCTTGTGAATTTTCTGAGAGGATGTACAAATACCTGAACATCATCAAC	840
Qy	841	CCAGTAATTAATGATTTTGAACACCACTGAGAACGCTGACGCTGAAGGATCCAGAAAAGT	900
Db	841	CCAGTAATTAATGATTTTGAACACCACTGAGAACGCTGACGCTGAAGGATCCAGAAAAGT	900
Qy	901	ATCAGGGTAGTTCGTGTTTCAAACTTGATGAGGCCATGTGAGCAAAATACCTATGCCA	960
Db	901	ATCAGGGTAGTTCGTGTTTCAAACTTGATGAGGCCATGTGAGCCAAATFACCTATGCCA	960
Qy	961	GCTCATTAACAGATAGAGAACGACGCTTTATTACTCATTAAGACAGAATGAATAGACAA	1020
Db	961	GCTCATTAACAGATAGAGAACGACGCTTTATTACTCATTAAGACAGAATGAATAGACAA	1020
Qy	1021	AGGCGAATTCGTAAATPAAAGCAAAACAGCGCTGCTTAGCAAGGAGCCAACTAAACGAT	1080
Db	1021	AGGCGAATTCGTAAATPAAAGCAAAACAGCGCTGCTTAGCAAGGAGCCAACTAAACGAT	1080
Qy	1081	GGGCTGAGAGTAGAGAAACATGATGATAGCGCGACTCCACAGACAGAAAAAAAGGTAG	1140
Db	1081	GGGCTGAGAGTAGAGAAACATGATGATAGCGCGACTCCACAGACAGAAAAAAAGGTAG	1140
Qy	1141	ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT	1200
Db	1141	ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT	1200
Qy	1201	CAGGAATTCCTAGAGATACCTGGAAGATGTCCTTGATTAACCTAAATAGCAGCTTGAGA	1260
Db	1201	CAGGAATTCCTAGAGATACCTGGAAGATGTCCTTGATTAACCTAAATAGCAGCTTGAGA	1260
Qy	1261	AAGTTAAATGAATGGTTTTTCCAGAAAGTATGAACTGTAGGTTCTGATGACTCACATGATG	1320
Db	1261	AAGTTAAATGAATGGTTTTTCCAGAAAGTATGAACTGTAGGTTCTGATGACTCACATGATG	1320
Qy	1321	GGGAGCTGGAATCAAAATCCAAAGTAGCTGATTTAGGACGTTCTAAATGAGGTAGTG	1380
Db	1321	GGGAGCTGGAATCAAAATCCAAAGTAGCTGATTTAGGACGTTCTAAATGAGGTAGTG	1380
Qy	1381	AATATTCGTGTTCTTCAGAGAAATATGACTTACCTGCGCAGAGATCCCTCATGAGCTTTAA	1440
Db	1381	AATATTCGTGTTCTTCAGAGAAATATGACTTACCTGCGCAGAGATCCCTCATGAGCTTTAA	1440
Qy	1441	TATGTAAAGTAGAAAGGATTCACTCCAAATCAGTAGAGAGTAATATTGAGACAAAAATAT	1500
Db	1441	TATGTAAAGTAGAAAGGATTCACTCCAAATCAGTAGAGAGTAATATTGAGACAAAAATAT	1500
Qy	1501	TTGGGAAAACTTATCGAGAGAAAGGCAAGCCCTCCCACTTAAGCCATGTAACCTGAAATC	1560
Db	1501	TTGGGAAAACTTATCGAGAGAAAGGCAAGCCCTCCCACTTAAGCCATGTAACCTGAAATC	1560
Qy	1561	TAAATTAATAGAGCACTTGTACTAGGCCACAGATTAATACAAAGACCGTCCCTCACAATA	1620
Db	1561	TAAATTAATAGAGCACTTGTACTAGGCCACAGATTAATACAAAGACCGTCCCTCACAATA	1620
Qy	1621	AATTAAGGCGTAAGAGGAGCACTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAAG	1680
Db	1621	AATTAAGGCGTAAGAGGAGCACTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAAG	1680

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QY 1741 AGAATGCTCAAGTGAATTAATTAATTAATGCTGCTAGGAATTAACCAAAAGTGATTC 1800
DB 1741 AGAATGCTCAAGTGAATTAATTAATTAATGCTGCTAGGAATTAACCAAAAGTGATTC 1800
QY 1801 CTATTCAGATGAGAAATATCTTAACCATAGAAATACCTCGAATAAAGATTCGCTTTC 1860
DB 1801 CTATTCAGATGAGAAATATCTTAACCATAGAAATACCTCGAATAAAGATTCGCTTTC 1860
QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTAAAGCAATATGAACTGAATTAATATCC 1920
DB 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTAAAGCAATATGAACTGAATTAATATCC 1920
QY 1921 ACAATTCAAAAGCACTTAAGAAATAGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
DB 1921 ACAATTCAAAAGCACTTAAGAAATAGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
QY 1981 ATGCGCTGAACCTAGTGAATGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2040
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DB 2401 AAAGATCTGTAAGAGTGAAGTATTTCACTGGTACCTGGTACTGATTAATGAGCACTCAG 2460
QY 2461 AAAGATCTGTAAGAGTGAAGTATTTCACTGGTACCTGGTACTGATTAATGAGCACTCAG 2520
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DB 3781 AAGAGCTTCCCTGCTTCAACCTGTTAATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3840
QY 3841 CTACTAAGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT 3900

Db	3841	CTACTAGGCATAGCACCGTTGCTTACCAGTGTCTGTCTTAGAACCAAGAGGAAATTTAT	3900
Oy	3901	TATCATTTAGAGATAGCTTTAAATGACTGCAGTAAACAGGTAAATATTTGGCAAGCATCTC	3960
Db	3901	TATCATTTAGAGATAGCTTTAAATGACTGCAGTAAACAGGTAAATATTTGGCAAGCATCTC	3960
Oy	3961	AGGAACATCACCTTTGTAGGGAACAACAAATGTTCTGTAGCTGTGTTTCTTCACAGTCA	4020
Db	3961	AGGAACATCACCTTTGTAGGGAACAACAAATGTTCTGTAGCTGTGTTTCTTCACAGTCA	4020
Oy	4021	GTGAATTTGGAAACCTTGACTGCAAAATACAAACACCAGAGTCCCTTCTTGATTTGGTTCCT	4080
Db	4021	GTGAATTTGGAAACCTTGACTGCAAAATACAAACACCAGAGTCCCTTCTTGATTTGGTTCCT	4080
Oy	4081	CCAAACAAATGAGCATCAGTCTGAAGCCAGGAGTTGGTCTGAGTCAAGAAATTGG	4140
Db	4081	CCAAACAAATGAGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTCAAGAAATTGG	4140
Oy	4141	TTTCAGATGATAGAAAGAGAAAGGGGCTTGGAAAGAAATATATCAAGAGCAACACA	4200
Db	4141	TTTCAGATGATAGAAAGAGAAAGGGGCTTGGAAAGAAATATATCAAGAGCAACACA	4200
Oy	4201	TGGATTCAAACTTACGTGAGCAGCATCTGGGTGTGAGGTGAACAAAGCGTCTGTGAAG	4260
Db	4201	TGGATTCAAACTTACGTGAGCAGCATCTGGGTGTGAGGTGAACAAAGCGTCTGTGAAG	4260
Oy	4261	ACTGTCAGGGGTATTCCTCTCAGATGACATTTTAACCACTCAGAGAGGATACCATGAC	4320
Db	4261	ACTGTCAGGGGTATTCCTCTCAGATGACATTTTAACCACTCAGAGAGGATACCATGAC	4320
Oy	4321	AAACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGAACCTGTGTAGAACACG	4380
Db	4321	AAACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGAACCTGTGTAGAACACG	4380
Oy	4381	ATGGAGGCCAGCCTTCTTAACAGCTACCTTCCATATAGTACATCTCTGCCCTTGAAG	4440
Db	4381	ATGGAGGCCAGCCTTCTTAACAGCTACCTTCCATATAGTACATCTCTGCCCTTGAAG	4440
Oy	4441	ACCTGCGAAATCCAGAACCAAGCAGATCAGAAAGAGATTAATCTTCAACAGAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACCAAGCAGATCAGAAAGAGATTAATCTTCAACAGAAAGTA	4500
Oy	4501	GTGAATACCCTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTTGAGGTCTG	4560
Db	4501	GTGAATACCCTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTTGAGGTCTG	4560
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Db	4561	CAGATAGTTCTACGAGTAAATTAAGAAACAGAGGTGGAAAGATCATCCCTCTTAAT	4620
Oy	4621	GCCCATCATTAAGATAGTGGTATGATGACAGAGTTGCTCTGGAGTCTTCAGAAATAGA	4680
Db	4621	GCCCATCATTAAGATAGTGGTATGATGACAGAGTTGCTCTGGAGTCTTCAGAAATAGA	4680
Oy	4681	ACTAACCATCTTAAGAGAGCTCATTTAAGTGTGTTGATGTGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTAACCATCTTAAGAGAGCTCATTTAAGTGTGTTGATGTGAGAGCAACAGCTGGAAG	4740
Oy	4741	AGTGTGGGACACACATTTGACGAAACATCTTAATCTTGCCAGAGCAAGATCTAGAGGAAA	4800
Db	4741	AGTGTGGGACACACATTTGACGAAACATCTTAATCTTGCCAGAGCAAGATCTAGAGGAAA	4800
Oy	4801	CCCTTTACCTGGAATCTGGAAATCAGCTCTTCTCTGATGACCTTAATCTGATCTCTTCTG	4860
Db	4801	CCCTTTACCTGGAATCTGGAAATCAGCTCTTCTCTGATGACCTTAATCTGATCTCTTCTG	4860
Oy	4861	AAGACAGAGCCCCAGAGTCAGTCTGTTGGGCAATACATCATCTTCAACTCTGATGTA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAGTCTGTTGGGCAATACATCATCTTCAACTCTGATGTA	4920
Oy	4921	AAGTTTCCCAATGAAGTTTGAGAAATCTGCCAGAGTCCAGCTGTGCTCACTACTGTG	4980
Db	4921	AAGTTTCCCAATGAAGTTTGAGAAATCTGCCAGAGTCCAGCTGTGCTCACTACTGTG	4980

D	b		4921	AAGTTCCCAATTGAAATTCGACGAATCTGCCACGGGTCCAGCTGTCCTACTACTG	4980
O	y		4981	ATACTGCTGGGTATTAATCCAATGGAAGAAGTGTGAGCAGGGAGAACCCAGAAATTGACG	5040
D	b		4981	ATACTGCTGGGTATTAATCCAATGGAAGAAGTGTGAGCAGGGAGAACCCAGAAATTGACG	5040
O	y		5041	CTTCAACGAAAGGGTCAAACAAAAGATGTCATCGTGCGTCTGGCCTGCACCAGAG	5100
D	b		5041	CTTCAACGAAAGGGTCAAACAAAAGATGTCATCGTGCGTCTGGCCTGCACCAGAG	5100
O	y		5101	AATTTATGCTCGTAGCAAGTTTTCACAAAAACACACATCATCTTAACTAATCTAATTA	5160
D	b		5101	AATTTATGCTCGTAGCAAGTTTTCACAAAAACACACATCATCTTAACTAATCTAATTA	5160
O	y		5161	CTGAAGACATCACTCATGTTGTTATGAAAAACAAGATCGTAATTTGTGTGTAACGGACAC	5220
D	b		5161	CTGAAGACATCACTCATGTTGTTATGAAAAACAAGATCGTAATTTGTGTGTAACGGACAC	5220
O	y		5221	TGAAATATATTTCTAGGAATTCGGGAGGAAAAATGGTAGTAGTATTTCTGGGTGACCC	5280
D	b		5221	TGAAATATATTTCTAGGAATTCGGGAGGAAAAATGGTAGTAGTATTTCTGGGTGACCC	5280
O	y		5281	AGTCTATTAAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATCTGG	5340
D	b		5281	AGTCTATTAAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATCTGG	5340
O	y		5341	TCAATGGAAGAAACCAACCAAGGTCCAAAGCAGACAAGAAATCCAGAGACGAAAGATCT	5400
D	b		5341	TCAATGGAAGAAACCAACCAAGGTCCAAAGCAGACAAGAAATCCAGAGACGAAAGATCT	5400
O	y		5401	TCAGGGGGCTAGAAATCTGTTGCTATGSGCCCTTTCACCAATGCCCCAGATCAATCG	5460
D	b		5401	TCAGGGGGCTAGAAATCTGTTGCTATGSGCCCTTTCACCAATGCCCCAGATCAATCG	5460
O	y		5461	AATGGATGGTACAGTGTGTGTGCTTGTGATGGAAGAGCTTTCAATCACTCACCCCTTG	5520
D	b		5461	AATGGATGGTACAGTGTGTGTGCTTGTGATGGAAGAGCTTTCAATCACTCACCCCTTG	5520
O	y		5521	GCACAGGTGTCCACCCAATTGTGTGTGTGACAGCAGATGCTTGACAGAGACAATGGCT	5580
D	b		5521	GCACAGGTGTCCACCCAATTGTGTGTGTGACAGCAGATGCTTGACAGAGACAATGGCT	5580
O	y		5581	TCCATGCAATTGGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGTGTGACA	5640
D	b		5581	TCCATGCAATTGGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGTGTGACA	5640
O	y		5641	GTTGAGCACTCTACAGTGCAGAGAGCTGACACACTACTGATACCCAGATCCCACCACA	5700
D	b		5641	GTTGAGCACTCTACAGTGCAGAGAGCTGACACACTACTGATACCCAGATCCCACCACA	5700
O	y		5701	GCCACTACTGA 5711	
D	b		5701	GCCACTACTGA 5711	
RESULT 11					
AAV46456 standard; cDNA; 5711 BP.					
XX	AC	AAV46456;			
XX	DT	18-NOV-1998	(first entry)		
XX	DE	Human BRCA1 omil polymorphism #6 cDNA.			
XX	KW	BRCA1; omil; human; breast and ovarian cancer predisposing gene;			
XX	KM	polymorphism; susceptibility; anti-oncogene; tumour suppressor;			
XX	OS	chromosome 17q; ss.			
XX	Key	Homo sapiens.			
XX	CDS	Location/Qualifiers			
XX	FT	120..5711			

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FT      /*tag= a
FT      /product= "BRCA1 om1 protein"
FT      4427
FT      Variation //tag= b
FT      /note= "This polymorphic variation can be a T or C
FT      nucleotide"
XX      US5750400-A.
XX      12-MAY-1998.
XX      12-FEB-1997; 97US-0798691.
XX      12-FEB-1996; 96US-0598591.
XX      12-FEB-1997; 97US-0798691.
XX      (ONCO-) ONCOMED INC.
XX      Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SU,
XX      Schelter DB, Zeng B;
XX      WPI; 1998-296774/26.
XX      BRCA1 om1 gene coding sequences - useful for distinguishing between
XX      polymorphisms and mutation(s) in the screening for disposition to
XX      breast or ovarian cancer
XX      Claim 2e; Page -; 54pp; English.
XX      This sequence encodes a human BRCA1 (breast and ovarian cancer
XX      predisposing gene) om1 gene in which a polymorphic variation occurs at
XX      nucleotide 4427. This sequence and other polymorphic variations of this
XX      sequence are useful for the identification of an individual who may or
XX      may not have an increased susceptibility to breast or ovarian cancer.
XX      The sequences used identify gene changes which are due to polymorphisms,
XX      rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX      suppressor) which is involved in genetic inheritance of cancers,
XX      especially breast and ovarian cancer. It is found at human chromosome
XX      17q which is known to be linked to cancer susceptibility, especially
XX      breast cancer. Cells containing a mutation in this gene lose the
XX      wild-type function of BRCA1 and are more susceptible to cancers.
XX      NOTE: This sequence does not appear in the specification but has been
XX      created from the wild type BRCA1 om1 gene represented in AAV46448.
XX      Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other:
XX      Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 AGCTCGCTGAGACTTCTCTGAGACCCGACGAGCTGTGGGTTTCTCAGATACTGGGC 60
DB      1 AGCTCGCTGAGACTTCTCTGAGACCCGACGAGCTGTGGGTTTCTCAGATACTGGGC 60
QY      61 CCTGCGCTGAGAGGCTTACCCCTCTGCTCTGGGTAAAGTTCATTGGAACAGAAAGAAA 120
DB      61 CCTGCGCTGAGAGGCTTACCCCTCTGCTCTGGGTAAAGTTCATTGGAACAGAAAGAAA 120
QY      121 TGAATTTATCTGCTCTTCCGCTTGAAGAAGTACAAAATGTCATTATGCTATGACAGAAA 180
DB      121 TGAATTTATCTGCTCTTCCGCTTGAAGAAGTACAAAATGTCATTATGCTATGACAGAAA 180
QY      181 TCTTAGAGTGTCCATCTGTCTGAGAGTGTATCAAGAACTGTCTCCACAAAGTGTGACC 240
DB      181 TCTTAGAGTGTCCATCTGTCTGAGAGTGTATCAAGAACTGTCTCCACAAAGTGTGACC 240
QY      241 ACATATTTTGGCAATTTTGGCATGCTGAACCTTCTCAACAGAAAGAGGCTTTCACAGT 300
DB      241 ACATATTTTGGCAATTTTGGCATGCTGAACCTTCTCAACAGAAAGAGGCTTTCACAGT 300
QY      301 GTCTTTATGTATGAATGATATTAACCAAAAGAGCTTACAGAAAGTACAGATTTAGTTC 360
DB      301 GTCTTTATGTATGAATGATATTAACCAAAAGAGCTTACAGAAAGTACAGATTTAGTTC 360

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QY      421 ATGCAAAACAGCTATAATTTTGGCAAAAAGAAAAATTAATCTCTCTGAACATCTAAAGATG 480
DB      421 ATGCAAAACAGCTATAATTTTGGCAAAAAGAAAAATTAATCTCTCTGAACATCTAAAGATG 480
QY      481 AAGTTTCTATCATCCAAAGATGAGGTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 540
DB      481 AAGTTTCTATCATCCAAAGATGAGGTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 540
QY      541 AACCCGAAATCCCTTCTTGACAGAAACAGCTCTGAGTCCAACTCTTAACTTTGGAA 600
DB      541 AACCCGAAATCCCTTCTTGACAGAAACAGCTCTGAGTCCAACTCTTAACTTTGGAA 600
QY      601 CTGTGAAACTGTGAGACCAAGACGAGTACAACTCAGAAAGAGTGTCTACATTTG 660
DB      601 CTGTGAAACTGTGAGACCAAGACGAGTACAACTCAGAAAGAGTGTCTACATTTG 660
QY      661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGCACTTATTCAGTGTGGAG 720
DB      661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAGCACTTATTCAGTGTGGAG 720
QY      721 ATCAAGAAATTTGTAACAAATCACCCCTCAAGAAACGAGGATGAAATCAGTTGGATTCTG 780
DB      721 ATCAAGAAATTTGTAACAAATCACCCCTCAAGAAACGAGGATGAAATCAGTTGGATTCTG 780
QY      781 CAAAAAGAGCTCTGTGTAATTTTCTGACAGGATGTAACTAATCTGAATCATCAAC 840
DB      781 CAAAAAGAGCTCTGTGTAATTTTCTGACAGGATGTAACTAATCTGAATCATCAAC 840
QY      841 CCAATATATATGTTTGAACACCACTGAGAACGCTGACCTGAGAGGCTTCCAGAAAGT 900
DB      841 CCAATATATATGTTTGAACACCACTGAGAACGCTGACCTGAGAGGCTTCCAGAAAGT 900
QY      901 ATCAGGATGTTCTGTGTAATTTTCTGACAGGATGTAACTAATCTGAATCATCAAC 960
DB      901 ATCAGGATGTTCTGTGTAATTTTCTGACAGGATGTAACTAATCTGAATCATCAAC 960
QY      961 GCTCATTTACAGATGAGAACACAGCTTATTAATCTCACTAAAGACAGAAATGTAGAAA 1020
DB      961 GCTCATTTACAGATGAGAACACAGCTTATTAATCTCACTAAAGACAGAAATGTAGAAA 1020
QY      1021 AAGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTACAGAGACCACTTAACAGAT 1080
DB      1021 AAGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTACAGAGACCACTTAACAGAT 1080
QY      1081 GGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGAGCTCCAGACAGAAAGAAAGGTAG 1140
DB      1081 GGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGAGCTCCAGACAGAAAGAAAGGTAG 1140
QY      1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAAATGAGCAAAATGCCATGCT 1200
DB      1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAAATGAGCAAAATGCCATGCT 1200
QY      1201 CAGAGAAATCTTGAAGTACTGAAGATGTTCTTGGATTAACATTAATAGCAGATTTCAGA 1260
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QY      1261 AAGTTAAGAGAGGTTTCTCAGAGAGTAACTGTGAGTCTGATGCTCAATGATG 1320
DB      1261 AAGTTAAGAGAGGTTTCTCAGAGAGTAACTGTGAGTCTGATGCTCAATGATG 1320
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Db 5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
QY 5641 GTGTAGCACTTACCAAGTGTGAGGCACTGTGTGTGATGATGATGATGATGATGATG 5700
Db 5641 GTGTAGCACTTACCAAGTGTGAGGCACTGTGTGTGATGATGATGATGATGATGATG 5700
QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 12
AAV46457
ID AAV46457 standard; cDNA; 5711 BP.

Db	1201	CAGAGAAATCTCGAGATACCTGAGATGTTCTTGATACCTAAATGCGAATTCAGA	1260
Qy	1261	AAGTTAATAGTGTGTTTTCCAGAAATGATGAACTGTGTTGTTGATGACTCACATGATG	1320
Db	1261	AAGTTAATAGATGTTTTCCAGAAATGATGAACTGTGTTGTTGATGACTCACATGATG	1320
Qy	1321	GGGAGTCTGAATCAATATCCAAAGTAGTGATGTAATTGGACGTTCTAAATGAGTAGATG	1380
Db	1321	GGGAGTCTGAATCAATATCCAAAGTAGTGATGTAATTGGACGTTCTAAATGAGTAGATG	1380
Qy	1381	AATATTCGTGTTCTCAGAGAAAAATAGACTTACCTGGCCAGATCCCATAGGCTTTAA	1440
Db	1381	AATATTCGTGTTCTCAGAGAAAAATAGACTTACCTGGCCAGATCCCATAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCACCTCCAATCAGTAGAGTAATATTGAAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCACCTCCAATCAGTAGAGTAATATTGAAGACAAATAT	1500
Qy	1501	TTGGGAAAAACCTATGGAGAAAGGCGACCTCCCAACTTAAGCCATGTAACTGAAAAATC	1560
Db	1501	TTGGGAAAAACCTATGGAGAAAGGCGACCTCCCAACTTAAGCCATGTAACTGAAAAATC	1560
Qy	1561	TAAATTATGAGACATTTGTTACTAGGCCACAGATATATCAAGAGCGTCCCTCAAAATA	1620
Db	1561	TAAATTATGAGACATTTGTTACTAGGCCACAGATATATCAAGAGCGTCCCTCAAAATA	1620
Qy	1621	AATTAAACGTPAAAGAGACCTACATCAGGCGTTCACTCGAGAGATTTTATCAAGAAAG	1680
Db	1621	AATTAAACGTPAAAGAGACCTACATCAGGCGTTCACTCGAGAGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTTGGACGTTCAAAAAGACTCCCTGAATGATTAATCAGGAACTTACCAAAACGAGC	1740
Db	1681	CAGATTTTGGACGTTCAAAAAGACTCCCTGAATGATTAATCAGGAACTTACCAAAACGAGC	1740
Qy	1741	AGAATGTGTCAAGTGTGAATTTACTAATAGTGTCAATGAGATTTAAACAAAGGTGATT	1800
Db	1741	AGAATGTGTCAAGTGTGAATTTACTAATAGTGTCAATGAGATTTAAACAAAGGTGATT	1800
Qy	1801	CTATTCAAAATGAGAAAAATCCTTAACCAATATGATATCCTGAAAAAGAAATCTGCTTCA	1860
Db	1801	CTATTCAAAATGAGAAAAATCCTTAACCAATATGATATCCTGAAAAAGAAATCTGCTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTATTAAGACGACATATTAAGCAATATGGAATCGAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTATTAAGACGACATATTAAGCAATATGGAATCGAATTAATATCC	1920
Qy	1921	ACAATTTCAAAAGCACCTTAAGAAATAGGCTGAGAGGAGAGTCTTCAACGAGCATATTC	1980
Db	1921	ACAATTTCAAAAGCACCTTAAGAAATAGGCTGAGAGGAGAGTCTTCAACGAGCATATTC	1980
Qy	1981	ATGCGCTTGAACCTAGTACTCAGTAGAATCTTAAGCCCACTTAATTGTATGTAATTGCAAA	2040
Db	1981	ATGCGCTTGAACCTAGTACTCAGTAGAATCTTAAGCCCACTTAATTGTATGTAATTGCAAA	2040
Qy	2041	TTGATAGTGTCTTAGCAGTGAAGATTAAGAAAAAAAAGTATCAACCAATATGCGACGTCA	2100
Db	2041	TTGATAGTGTCTTAGCAGTGAAGATTAAGAAAAAAAAGTATCAACCAATATGCGACGTCA	2100
Qy	2101	GGCAGCAGAGAAACCTTACACTCATGAAAGGTAAAGAACTTGCAACTGAGACCAAGAAAGA	2160
Db	2101	GGCAGCAGAGAAACCTTACACTCATGAAAGGTAAAGAACTTGCAACTGAGACCAAGAAAGA	2160
Qy	2161	GTAACAAACCCAAATGAACAGACAAATGAACATGACATGATATCTTTCCCAAGGTGA	2220
Db	2161	GTAACAAACCCAAATGAACAGACAAATGAACATGACATGATATCTTTCCCAAGGTGA	2220
Qy	2221	AGTTAAACAAATGACACTGTTCTTTACTTAAGTGTCAAAATACCGAGTGAATTTAAAGAT	2280
Db	2221	AGTTAAACAAATGACACTGTTCTTTACTTAAGTGTCAAAATACCGAGTGAATTTAAAGAT	2280
Qy	2281	TTGTCAATCTTACGCTTCCAAAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTTACGCTTCCAAAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT	2340

Db	2281	TTGTCATCTCTAGCCTTCCAAGAGACAAAAAGAGAAACTTGTGAAACAGTTAAAGCT	2340
QY	2341	CTAATTAATGCTGAAGACCCCAAGACTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAGACTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG	2400
QY	2401	AAAGATCTGTAGAGATGACAGTATTTCACTGGTAACTGGTACTGATTAATGCACTAGG	2460
Db	2401	AAAGATCTGTAGAGATGACAGTATTTCACTGGTAACTGGTACTGATTAATGCACTAGG	2460
QY	2461	AAAGATCTGTTACTGGAAAGTTGCACTGAGGGAAGGCAAAAACGAACCAATTAAT	2520
Db	2461	AAAGATCTGTTACTGGAAAGTTGCACTGAGGGAAGGCAAAAACGAACCAATTAAT	2520
QY	2521	GTGTGAGTCAGTGTGACAGCACTTTGAAAAACCCCAAGGCACTAATTCATGTTGTTCCAAG	2580
Db	2521	GTGTGAGTCAGTGTGACAGCACTTTGAAAAACCCCAAGGCACTAATTCATGTTGTTCCAAG	2580
QY	2581	ATTAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGACATGAAGTTAACCAAGTC	2640
Db	2581	ATTAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGACATGAAGTTAACCAAGTC	2640
QY	2641	GGGAAAACAAGATNGAAATGGAGAAAGTGAACCTGATGCTCACTATTTGCAAAATCAT	2700
Db	2641	GGGAAAACAAGATNGAAATGGAGAAAGTGAACCTGATGCTCACTATTTGCAAAATCAT	2700
QY	2701	TCAAGGTTTCAAAACGCGCAGTCACTTGTCTCGTTTTCAAATCCGAGAAATGACAAAGG	2760
Db	2701	TCAAGGTTTCAAAACGCGCAGTCACTTGTCTCGTTTTCAAATCCGAGAAATGACAAAGG	2760
QY	2761	AATGTGCAACATTCCTGCCCCACTCTGAGGTCCTTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAACATTCCTGCCCCACTCTGAGGTCCTTTAAAGAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGAATGTGAAACAAAGAGAGAAAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAAACAAAGAGAGAAAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC	2880
QY	2881	AGACAGTTAATATCACTGCAAGGCTTCTGCGTGGTGTGTCAGAAAGATPAAGCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGCAAGGCTTCTGCGTGGTGTGTCAGAAAGATPAAGCAGTTGATA	2940
QY	2941	ATGCGCAATGTAGTATCAAAAGAGGCTCTAAGGTTTTGTCATATCATCTCAGTTCAAGACA	3000
Db	2941	ATGCGCAATGTAGTATCAAAAGAGGCTCTAAGGTTTTGTCATATCATCTCAGTTCAAGACA	3000
QY	3001	ACGAAACTGCACTCATTTACTCCAAATTAACATGACCTTTTACAAAACCCATATCTGTATAC	3060
Db	3001	ACGAAACTGCACTCATTTACTCCAAATTAACATGACCTTTTACAAAACCCATATCTGTATAC	3060
QY	3061	CACGACCTTTTCCCATPAAGTCATTTGTATTAATGTAAATGTAAAGAAAAATCTGTAGAGG	3120
Db	3061	CACGACCTTTTCCCATPAAGTCATTTGTATTAATGTAAATGTAAAGAAAAATCTGTAGAGG	3120
QY	3121	AAAACTTTGAGAAACATTCAATGTCACTGCACTGTAAGAGAGAAATGAGAAACATTCCAA	3180
Db	3121	AAAACTTTGAGAAACATTCAATGTCACTGCACTGTAAGAGAGAAATGAGAAACATTCCAA	3180
QY	3181	GTACAGTGACACAAATTAGCCGTATATACATTVAGAGAAAAATGTTTTTAATAGAGCCAGCT	3240
Db	3181	GTACAGTGACACAAATTAGCCGTATATACATTVAGAGAAAAATGTTTTTAATAGAGCCAGCT	3240
QY	3241	CAACCAATTTAATAGAGTAGTGGTCCAGTACTAATGAGAGGCGTCAGATTAATAGAA	3300
Db	3241	CAACCAATTTAATAGAGTAGTGGTCCAGTACTAATGAGAGGCGTCAGATTAATAGAA	3300
QY	3301	TAGGTTTCAGTGTATGAANAACATTCAAGCACAACCTAGTAAACACAGAGGCCCAAAATTGA	3360
Db	3301	TAGGTTTCAGTGTATGAANAACATTCAAGCACAACCTAGTAAACACAGAGGCCCAAAATTGA	3360
QY	3361	ATGCTATGCTTAAAGTTAAGGAGTTTTTGCAACCTGAAGCTATTAACAAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAAAGTTAAGGAGTTTTTGCAACCTGAAGCTATTAACAAAGTCTTCTGGAA	3420

QY 3421 GTAATTGTAAGCTTCTGAAATTAATAAAGCAAGAAATATGAGAAGTACTGACACTGTTA 3480
Db 3421 GTAATTGTAAGCATCTCTAAATAAATAAAGCAAGAAATATGAGAAGTACTGACACTGTTA 3480
QY 3481 ATACAGATTTTCTCTCATATCTGATTTGATTAACCTAGTAAGACAGCTTATGGAAGTATGTC 3540
Db 3481 ATACAGATTTTCTCTCATATCTGATTTGATTAACCTAGTAAGACAGCTTATGGAAGTATGTC 3540
QY 3541 ATGCACTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGATGATTAAGG 3600
Db 3541 ATGCACTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGATGATTAAGG 3600
QY 3601 AAGTACTAGTTTGTGTAATAATGACATTAAGAAAGTTCTGCTGTTTATACAAAGG 3660
Db 3601 AAGTACTAGTTTGTGTAATAATGACATTAAGAAAGTTCTGCTGTTTATACAAAGG 3660
QY 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG 3720
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG 3720
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTAGAGATG 3780
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTAGAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAGTAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAGTAACAATATACCTTCTCAGT 3840
QY 3841 CTACTAGGATAGACACCGTTCCTAGCAGTGTCTGCTTAAAGAACAGAGAGAAATTTAT 3900
Db 3841 CTACTAGGATAGACACCGTTCCTAGCAGTGTCTGCTTAAAGAACAGAGAGAAATTTAT 3900
QY 3901 TATCATTGAAGATATGCTTAAATGACTGCAATACCAAGTAATATTGGCAAGGCAATCTC 3960
Db 3901 TATCATTGAAGATATGCTTAAATGACTGCAATACCAAGTAATATTGGCAAGGCAATCTC 3960
QY 3961 AGGAACATCACCTTGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
Db 3961 AGGAACATCACCTTGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
QY 4021 GTGAATTGGAAGACTTGACTGCAATACCAACACCCAGAGTCTTCTTGTATGTTCTT 4080
Db 4021 GTGAATTGGAAGACTTGACTGCAATACCAACACCCAGAGTCTTCTTGTATGTTCTT 4080
QY 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCAGGAGTTGGTCTGAGTGAACAAGAAATGG 4140
Db 4081 CCAAAACAAATGAGGATCAGTCTGAAAGCAGGAGTTGGTCTGAGTGAACAAGAAATGG 4140
QY 4141 TTTCAAGATGATGAAGAAAGAGAGCGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200
Db 4141 TTTCAAGATGATGAAGAAAGAGAGCGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200
QY 4201 TGAATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCTCTCTGAG 4260
Db 4201 TGAATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCTCTCTGAG 4260
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACCACTCAGAGAGAGGAGTACCATG 4320
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAAACCACTCAGAGAGAGGAGTACCATG 4320
QY 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGGCTGAATAGAGTGTGTAAGAACAGC 4380
Db 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGGCTGAATAGAGTGTGTAAGAACAGC 4380
QY 4381 ATGGAGCCAGGCTTCTAAGAGCTACCTTCCATCATTAAGTACTCTTCTGCTTGAAG 4440
Db 4381 ATGGAGCCAGGCTTCTAAGAGCTACCTTCCATCATTAAGTACTCTTCTGCTTGAAG 4440
QY 4441 ACCTGCGAAATCCAGAAACAAAGACATCAGAAAAGAGATTTAACTTACAGAAAAGTA 4500
Db 4441 ACCTGCGAAATCCAGAAACAAAGACATCAGAAAAGAGATTTAACTTACAGAAAAGTA 4500

QY 4501 GTGAATACCTTATAGCCAGAAATCCAGAGGCCCTTCTGCTGACCAAGTTTGAAGTGTCTG 4560
Db 4501 GTGAATACCTTATAGCCAGAAATCCAGAGGCCCTTCTGCTGACCAAGTTTGAAGTGTCTG 4560
QY 4561 CAGATAGTTCTTACAGTAAATAAAGAACCCAGAGTGAAGAGTCAATCCCTTCTTAAAT 4620
Db 4561 CAGATAGTTCTTACAGTAAATAAAGAACCCAGAGTGAAGAGTCAATCCCTTCTTAAAT 4620
QY 4621 GCCCATCTTATGATGATGAGTGTGATCAATGACAGTTCCTGAGAGTCTTCAAGATTAAG 4680
Db 4621 GCCCATCTTATGATGATGAGTGTGATCAATGACAGTTCCTGAGAGTCTTCAAGATTAAG 4680
QY 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGTAAGTGTGAGAGAACCAAGCTGGAAG 4740
Db 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGTAAGTGTGAGAGAACCAAGCTGGAAG 4740
QY 4741 AGTCTGGGCCACACGATTTGACGGAACATCTTAATCTTCCAGAGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCCACACGATTTGACGGAACATCTTAATCTTCCAGAGCAAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAATCTGGAATTCAGCTCTTCTGATGACCCCTGAATCTGATCTTCTG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATTCAGCTCTTCTGATGACCCCTGAATCTGATCTTCTG 4860
QY 4861 AAGACAGAGCCCCAGAGTCAAGCTGTGTTGGCAACATACCATCTTCAACCTTGCAATTA 4920
Db 4861 AAGACAGAGCCCCAGAGTCAAGCTGTGTTGGCAACATACCATCTTCAACCTTGCAATTA 4920
QY 4921 AAGTTCCCAATTGAAGTTGACAGAAATCTGCCAGAGGCTCAGCTGCTCTCATTAATCTG 4980
Db 4921 AAGTTCCCAATTGAAGTTGACAGAAATCTGCCAGAGGCTCAGCTGCTCTCATTAATCTG 4980
QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAGTGTGACAGAGGAGGAGCCGAATTAAG 5040
Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAGTGTGACAGAGGAGGAGCCGAATTAAG 5040
QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGAGCTGACCCAGAAAG 5100
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGAGCTGACCCAGAAAG 5100
QY 5101 AATTATGCTGTGTACAAAGTTTCCAGAAACACCAATCATCTTAACTTAATCTTAATTA 5160
Db 5101 AATTATGCTGTGTACAAAGTTTCCAGAAACACCAATCATCTTAACTTAATCTTAATTA 5160
QY 5161 CTGAAGAGATCACTCATGTTGTTATGAAGACAGATGCTGAGTTGTGTGAAACGAGCAC 5220
Db 5161 CTGAAGAGATCACTCATGTTGTTATGAAGACAGATGCTGAGTTGTGTGAAACGAGCAC 5220
QY 5221 TGAATATATTTCTAGAAATGCGGAGAGAAATGGTAGTTAGCTATTTCTGGGTGACCC 5280
Db 5221 TGAATATATTTCTAGAAATGCGGAGAGAAATGGTAGTTAGCTATTTCTGGGTGACCC 5280
QY 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340
Db 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340
QY 5341 TCAATGGAAGAACACCAAGGCTCAAGAGAGAGAGAGAAATCCCAAGAGAGAAAGTCT 5400
Db 5341 TCAATGGAAGAACACCAAGGCTCAAGAGAGAGAGAGAGAAATCCCAAGAGAGAAAGTCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATAGGAGCTTCAACCAATGCCCCAGATCAACTGG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATAGGAGCTTCAACCAATGCCCCAGATCAACTGG 5460
QY 5461 AATGATGTAACAGCTGTGTGCTCTCTGTGTGTAAGAGCTTCAATTAACCTTGG 5520
Db 5461 AATGATGTAACAGCTGTGTGCTCTCTGTGTGTAAGAGCTTCAATTAACCTTGG 5520
QY 5521 GCACAGGTCACACCAATTTGTGTGTGACAGCAGATGCTGGACAGAGAGCAATGGCT 5580
Db 5521 GCACAGGTCACACCAATTTGTGTGTGACAGCAGATGCTGGACAGAGAGCAATGGCT 5580
QY 5581 TCCATGCAATTTGGGACAGATGTGTGAGGACCTGTGTGTGACCCAGAGAGTGGGTGTGACA 5640

Db 5581 TCCATGCAATTGGCGAGATGTGAGGACCTGTGATGCCAGAGTGGGTGGACA 5640
QY 5641 GTTAGACACTCTCCAGTGCAGAGAGTGCACCTATCCGATATCCCAATCCCCACA 5700
Db 5641 GTTAGACACTCTCCAGTGCAGAGAGTGCACCTATCCGATATCCCAATCCCCACA 5700
QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 13
AAV46450 standard; cDNA; 5711 BP.
XX AAV46450;
AC AAV46450;
XX
XX 18-NOV-1998 (first entry)
DE Human BRCA1 om13 cDNA.
XX
XX BRCA1; om13; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT /*tag= a
FT /*product= "BRCA1 om13 protein"
XX
PN US5750400-A.
XX
PD 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-0798691.
PF
XX
PR 12-FEB-1996; 96US-0598591.
PR 12-FEB-1997; 97US-0798691.
XX
XX (ONCO-) ONCORMED INC.
PA
XX
PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ.
PI Schelter DB, Zeng B;
XX
DR WPI; 1998-296774/26.
DR P-PSDB; AAW76100.
XX
XX BRCA1 om1 gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
XX Claim 2e; Column 55-62; 54pp; English.
XX
XX This sequence encodes the human BRCA1 (breast and ovarian cancer
XX predisposing gene) om13 gene. This sequence and polymorphic variations of
XX this sequence are useful for the identification of an individual who may
XX or may not have an increased susceptibility to breast or ovarian cancer.
XX The sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome 17q
XX which is known to be linked to cancer susceptibility, especially breast
XX cancer. Cells containing a mutation in this gene lose the wild-type
XX function of BRCA1 and are more susceptible to cancers.
XX
XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
Db 1 AGCTGCTGAGACTTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
QY 61 CCTGCGCTCAGAGAGGCTTCACTCTGCTGTGGTAAAGTTTATTGGAACAGAAAGAA 120
Db 61 CCTGCGCTCAGAGAGGCTTCACTCTGCTGTGGTAAAGTTTATTGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTGGCGCTTGAAGAATACAAATGTCATTATGCTATGCAAGAA 180
Db 121 TGGATTATCTGCTCTTGGCGCTTGAAGAATACAAATGTCATTATGCTATGCAAGAA 180
QY 181 TCTTAGAGTGCCTCATCTGCTGAGAGTGTATCAAGGAACCTGTCTCAAAAGTGTAGCC 240
Db 181 TCTTAGAGTGCCTCATCTGCTGAGAGTGTATCAAGGAACCTGTCTCAAAAGTGTAGCC 240
QY 241 ACATATTTTGCAGAAATTTTGCATGCTGAGAACTTCTCAACAGAGAAAGAGGCTTCAAGT 300
Db 241 ACATATTTTGCAGAAATTTTGCATGCTGAGAACTTCTCAACAGAGAAAGAGGCTTCAAGT 300
QY 301 GTTCCTTATGTAAGATGATATATACCAAGAGAGCTTACAGAAATAGATTTAGTC 360
Db 301 GTTCCTTATGTAAGATGATATATACCAAGAGAGCTTACAGAAATAGATTTAGTC 360
QY 361 AACTGTGAGAGCTATTTGAGAAATCATTTGTGCTTTTCAAGCTTGACACAGTTTGGAGT 420
Db 361 AACTGTGAGAGCTATTTGAGAAATCATTTGTGCTTTTCAAGCTTGACACAGTTTGGAGT 420
QY 421 ATGCAAAACAGTATATATTTTGCAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480
Db 421 ATGCAAAACAGTATATATTTTGCAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAGAACTTTACAGAGT 540
Db 481 AAGTTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAGAACTTTACAGAGT 540
QY 541 AACCCGAAATCCTTCTCTGAGAGAAACAGTCTCAGTGTCCAACTCTGAACCTTGGAA 600
Db 541 AACCCGAAATCCTTCTCTGAGAGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
QY 601 CTGTGAGAACTCTGAGAGCAAGACGAGTACCACTTCAAAAGAGCTGTCTATCATTTG 660
Db 601 CTGTGAGAACTCTGAGAGCAAGACGAGTACCACTTCAAAAGAGCTGTCTATCATTTG 660
QY 661 AATTGGATCTGATTTCTTGAAGATACCGTTATATAGCAACTTATTGCAAGTGGAG 720
Db 661 AATTGGATCTGATTTCTTGAAGATACCGTTATATAGCAACTTATTGCAAGTGGAG 720
QY 721 ATCAAGATTTGTAACAATCACCCCTCAAGAGAACAGGAGTGAATCAGTTGGATTCTG 780
Db 721 ATCAAGATTTGTAACAATCACCCCTCAAGAGAACAGGAGTGAATCAGTTGGATTCTG 780
QY 781 CAAAAAAGGCTCTGTGTAATTTTCTGAGACGAGTGTAACAATACTGAATCATCAAC 840
Db 781 CAAAAAAGGCTCTGTGTAATTTTCTGAGACGAGTGTAACAATACTGAATCATCAAC 840
QY 841 CAGATATATATTTGAAACACCACTGAGAACGCTGACCTGAGAGCATCCAGAAAGT 900
Db 841 CAGATATATATTTGAAACACCACTGAGAACGCTGACCTGAGAGCATCCAGAAAGT 900
QY 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGAGCATGTGGCACTCAATATCATGCA 960
Db 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGAGCATGTGGCACTCAATATCATGCA 960
QY 961 GCTCATTTACAGATGAGAACAGCAGTTATTACTCACTAAACAGAAATGATGAGAA 1020
Db 961 GCTCATTTACAGATGAGAACAGCAGTTATTACTCACTAAACAGAAATGATGAGAA 1020
QY 1021 AGGCTGAATTTCTGATATAAAGCAACAGCTGTGCTAGCAAGAGCCCAACTAACAT 1080
Db 1021 AGGCTGAATTTCTGATATAAAGCAACAGCTGTGCTAGCAAGAGCCCAACTAACAT 1080

QY 1081 GGGCTGGAAGTAAGGAAACATGTATGATAGGGGGGCTCCAGACACAGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAGGAAACATGTATGATAGGGGGGCTCCAGACACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAGAGAAAGTCCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAGAGAAAGTCCATGCT 1200
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATACACTTAATAGACATTTGAGA 1260
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGGATACACTTAATAGACATTTGAGA 1260
QY 1261 AAGTTAATGAGAGGTTTTCCAGAGATGAAGTCTAGGTTCTGATGATGATGATGATG 1320
DB 1261 AAGTTAATGAGAGGTTTTCCAGAGATGAAGTCTAGGTTCTGATGATGATGATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGACGTTCTAAATGAGATGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGACGTTCTAAATGAGATGATG 1380
QY 1381 AATATTCCTGTTCTTCAGAGAAATAGACTTACGCGCCAGTATCTCTCATGAGCTTTAA 1440
DB 1381 AATATTCCTGTTCTTCAGAGAAATAGACTTACGCGCCAGTATCTCTCATGAGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGATTCTCAATCAGTAGAGATATATTGAAGCAAAATAT 1500
DB 1441 TATGTAAAGTGAAGAGATTCTCAATCAGTAGAGATATATTGAAGCAAAATAT 1500
QY 1501 TTGGGAAAACTGTGGAAGAGGCAAGGCTCCCACTTAAAGCCATGTAAGTGAAGATC 1560
DB 1501 TTGGGAAAACTGTGGAAGAGGCAAGGCTCCCACTTAAAGCCATGTAAGTGAAGATC 1560
QY 1561 TAAATATGAGAGATTTGTTACTGAGCCACAGATATACAGAGGCTCCCTCACAAATA 1620
DB 1561 TAAATATGAGAGATTTGTTACTGAGCCACAGATATACAGAGGCTCCCTCACAAATA 1620
QY 1621 AATTAAAGCGTAAAGAGAGACTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
DB 1621 AATTAAAGCGTAAAGAGAGACTTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTTAAACGAGAC 1740
DB 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTTAAACGAGAC 1740
QY 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTCATAGAGATTAAGAGAGGATGAT 1800
DB 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTCATAGAGATTAAGAGAGGATGAT 1800
QY 1801 CTATTCAGAAATGAGAAAAATCTTAACCCATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860
DB 1801 CTATTCAGAAATGAGAAAAATCTTAACCCATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860
QY 1861 AAAAGAAAGCTGAACCTATAGCAGATATAGCAATATGAGAACTCGAATTAATATCC 1920
DB 1861 AAAAGAAAGCTGAACCTATAGCAGATATAGCAATATGAGAACTCGAATTAATATCC 1920
QY 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAAAGTCTTCTACAGGCAATATC 1980
DB 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAAAGTCTTCTACAGGCAATATC 1980
QY 1981 ATGCGCTTGAATAGTACTAGTGAAGAAATCTAAGCCCACTAATTTGATCTGAATGGCAA 2040
DB 1981 ATGCGCTTGAATAGTACTAGTGAAGAAATCTAAGCCCACTAATTTGATCTGAATGGCAA 2040
QY 2041 TTGATAGTTGTTCTGACAGTGAAGATTAAGAAAAAAGTAAACCAATGCGAGTCA 2100
DB 2041 TTGATAGTTGTTCTGACAGTGAAGATTAAGAAAAAAGTAAACCAATGCGAGTCA 2100
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DB 2101 GGCACAGAGAGAAACCTTACACACTCAGAGAGTAAAGAACTCTGCACTGAGGCGAAGAAA 2160
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DB 5701 GCCACTACTGA 5711

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RESULT 15

AAV46465
AAV46465 standard, cDNA; 5711 BP.

AAV46465;

18-NOV-1998 (first entry)

Human BRCA1 omi3 polymorphism #1 cDNA.

BRCA1; omi3; human; breast and ovarian cancer predisposing gene;

KM polymorphism; susceptibility; anti-oncogene; tumour suppressor;

XX chromosome 17q; ss.

OS Homo sapiens.

XX

XX

XX

XX

XX

XX

XX

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XX

XX

XX

XX

XX

```

XX BRCA1 omi gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
XX Claim 2e; Page -; 54pp; English.
XX
CC This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
CC nucleotide 2201. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi3 gene represented in AAV46450.
XX
XX Sequence 5711 BP, 1953 A; 1098 C; 1277 G; 1382 T; 1 other;
SQ

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Query Match 100.0%; Score 5709; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5709; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 AGCTGCTGAGACCTTCCTGAGCCCGACAGAGCTGTGGGTTTCTCAGATTAATCTGGGCC 60

QY 61 CCTGGGCTCAGAGAGGCTTCAACCTGCTCTGGGTAAGTTCATTTGAAACGAAAGAA 120

DB 61 CCTGGGCTCAGAGAGGCTTCAACCTGCTCTGGGTAAGTTCATTTGAAACGAAAGAA 120

QY 121 TGGATTTATCTGCTCTGCGCTTGAAGAGTCAAAATGCTATTAATGATGACAGAAA 180

DB 121 TGGATTTATCTGCTCTGCGCTTGAAGAGTCAAAATGCTATTAATGATGACAGAAA 180

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DB 181 TCTTGAAGTGTCCATCTGTCTGAGTGTATGAAGAACCTGTCTTCAAAAGTGTACC 240

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Job time : 1122 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:59:20 ; Search time 720.5 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	9	US-09-734-672-3
2	5711	100.0	5711	9	US-09-982-828-5
3	5703	99.9	5711	9	US-09-734-672-5
4	5703	99.9	5711	9	US-09-982-828-3
5	5703	99.9	5711	9	US-10-022-819-1
6	5701.4	99.8	5711	9	US-09-734-672-1
7	5701.4	99.8	5711	9	US-09-982-828-1
8	364.6	6.4	499	9	US-09-911-904-127
9	175.4	3.1	424	10	US-09-864-761-4552
10	147	2.6	147	10	US-09-864-761-21299
11	121	2.1	121	9	US-09-818-875-653
12	121	2.1	121	9	US-09-818-875-654
13	121	2.1	121	9	US-09-818-875-657
14	121	2.1	121	9	US-09-818-875-658
15	121	2.1	121	9	US-09-818-875-661
16	121	2.1	121	9	US-09-818-875-662
17	121	2.1	121	9	US-09-818-875-665
18	121	2.1	121	9	US-09-818-875-666
19	121	2.1	121	9	US-09-818-875-669

C 20	121	2.1	121	9	US-09-818-875-670	Sequence 670, App
C 21	121	2.1	121	9	US-09-818-875-673	Sequence 673, App
C 22	121	2.1	121	9	US-09-818-875-674	Sequence 674, App
C 23	121	2.1	121	9	US-09-818-875-677	Sequence 677, App
C 24	121	2.1	121	9	US-09-818-875-678	Sequence 678, App
C 25	121	2.1	121	9	US-09-818-875-681	Sequence 681, App
C 26	121	2.1	121	9	US-09-818-875-682	Sequence 682, App
C 27	121	2.1	121	9	US-09-818-875-685	Sequence 685, App
C 28	121	2.1	121	9	US-09-818-875-686	Sequence 686, App
C 29	121	2.1	121	9	US-09-818-875-689	Sequence 689, App
C 30	121	2.1	121	9	US-09-818-875-690	Sequence 690, App
C 31	121	2.1	121	9	US-09-818-875-693	Sequence 693, App
C 32	121	2.1	121	9	US-09-818-875-694	Sequence 694, App
C 33	121	2.1	121	9	US-09-818-875-697	Sequence 697, App
C 34	121	2.1	121	9	US-09-818-875-698	Sequence 698, App
C 35	121	2.1	121	9	US-09-818-875-701	Sequence 701, App
C 36	121	2.1	121	9	US-09-818-875-702	Sequence 702, App
C 37	121	2.1	121	9	US-09-818-875-705	Sequence 705, App
C 38	121	2.1	121	9	US-09-818-875-706	Sequence 706, App
C 39	121	2.1	121	9	US-09-818-875-709	Sequence 709, App
C 40	121	2.1	121	9	US-09-818-875-710	Sequence 710, App
C 41	121	2.1	121	9	US-09-818-875-713	Sequence 713, App
C 42	121	2.1	121	9	US-09-818-875-714	Sequence 714, App
C 43	121	2.1	121	9	US-09-818-875-717	Sequence 717, App
C 44	121	2.1	121	9	US-09-818-875-718	Sequence 718, App
C 45	121	2.1	121	9	US-09-818-875-721	Sequence 721, App

ALIGNMENTS

RESULT 1
US-09-734-672-3
Sequence 3, Application US/09734672
Publication No. US20020183268A1
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
Allen, Antonette C.
Alvarez, Christopher P.
Critz, Brenda S.
Olson, Sheri J.
Schelter, Denise B.
Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Ave., N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,672
FILING DATE: 03-Dec-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/966,436
FILING DATE: 07-NO. US20020183268A1-97
APPLICATION NUMBER: US 08/598,591
FILING DATE: 12-Feb-96
ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44921-5055-02-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20020183268A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
us-09-734-672-3

Query Match 100.0%; Score 5711; DB 9; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1261 AAGTTAATGAGTGTTCCTCAGAAAGTGAAGTGTTCCTTGAATACACTAATATGAC 1320
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1321 GGGAGTCTGAATCAATCCAAAGTGAAGTGTTCCTTGAATACACTAATATGAC 1380
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Db	1921	ACAAATTTCAAAGCAGCTTAATAAAGATAGCGTAGAGGAGAGTCTTCTACCGCAGCATATTC	1980
QY	1981	ATGGCGCTTGAACCTACTAGTCAGGTAAATATCTAAGCCCACTAATTTGTACTGAATTGCAA	2040
Db	1981	ATGGCGCTTGAACCTACTAGTCAGGTAAATATCTAAGCCCACTAATTTGTACTGAATTGCAA	2040
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Db	2041	TTGATAGTTGTTCTCTAGCAGTGAAGAGATPAAGAAAAAAGATACACCAATATGCGCAGTCA	2100
QY	2101	GGCAGCAGAGAAACCTACACTCATGGAAGGTAAGAACTTGCAACTGAGACCAGAAAGA	2160
Db	2101	GGCAGCAGAGAAACCTACACTCATGGAAGGTAAGAACTTGCAACTGAGACCAGAAAGA	2160
QY	2161	GTAACAACGCCAAATGGAACAGACAACTAATAAGACATGACAGGATPCTTTCCACAGCTGA	2220
Db	2161	GTAACAACGCCAAATGGAACAGACAACTAATAAGACATGACAGGATPCTTTCCACAGCTGA	2220
QY	2221	AGTTAAACAATGACACCTGGTCTTTTACTAAGTGTCAATATACGAGTAACTTTAAAGAT	2280
Db	2221	AGTTAAACAATGACACCTGGTCTTTTACTAAGTGTCAATATACGAGTAACTTTAAAGAT	2280
QY	2281	TTGTCAATCTAGCGCTTCCAGAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTAGCGCTTCCAGAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT	2340
QY	2341	CTAATATATGCTGAGAGACCCCAAAGATCTCATGTTAAGTGGAGAAAGGGTTTGCAACTG	2400
Db	2341	CTAATATATGCTGAGAGACCCCAAAGATCTCATGTTAAGTGGAGAAAGGGTTTGCAACTG	2400
QY	2401	AAAGATCTGTAAGAGTAGACAGTATTTCAATGGTACCGATGATATATGCGACTCAGG	2460
Db	2401	AAAGATCTGTAAGAGTAGACAGTATTTCAATGGTACCGATGATATATGCGACTCAGG	2460
QY	2461	AAAGATCTGTAAGTAGAGTTAGCACTTAGGGAGGCAAAACACAAACCAATTAAT	2520
Db	2461	AAAGATCTGTAAGTAGAGTTAGCACTTAGGGAGGCAAAACACAAACCAATTAAT	2520
QY	2521	GTTGTAAGTCAAGTGTGACAGATTTTGAAAACCCAAGGGACATTAATCATGGTGTTCAAAG	2580
Db	2521	GTTGTAAGTCAAGTGTGACAGATTTTGAAAACCCAAGGGACATTAATCATGGTGTTCAAAG	2580
QY	2581	ATATATAGAAATGACACAGAGGCTTTAGTATCCATTGGGACATGAAGTTAACCAAGCTC	2640
Db	2581	ATATATAGAAATGACACAGAGGCTTTAGTATCCATTGGGACATGAAGTTAACCAAGCTC	2640
QY	2641	GGGAACAACAGCATATGAATAATGAGAACAAAGTGAATGTATGATTTTGACAGAAATCAT	2700
Db	2641	GGGAACAACAGCATATGAATAATGAGAACAAAGTGAATGTATGATTTTGACAGAAATCAT	2700
QY	2701	TCAAAGTTTCAAAGCGCCAGTCAITTTGCTGTGTTTCAAATCCAGAAATGACAGAAAGG	2760
Db	2701	TCAAAGTTTCAAAGCGCCAGTCAITTTGCTGTGTTTCAAATCCAGAAATGACAGAAAGG	2760
QY	2761	AATGTGCAACATTTCTGTGCCCACTCTGGGTCTTTAAACAAACCAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGTGCCCACTCTGGGTCTTTAAACAAACCAAGTCCAAAGTCACTT	2820
QY	2821	TTGAATGTGAACAAAGAGAGAAATAATCAAGAAAGATGAAGTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAGAGAAATAATCAAGAAAGATGAAGTCTTAATATCAAGCTGTAC	2880
QY	2881	AGACAGTTAATATCACTGACGAGCTTTCTGTGGTTGGTCAAGAAAGATPAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGACGAGCTTTCTGTGGTTGGTCAAGAAAGATPAAGCCAGTTGATA	2940
QY	2941	ATGCCAAATGTATGATCAAAAGAGGCTTACGTTTGTCTATCATCTTCAGTTCCAGAGCA	3000
Db	2941	ATGCCAAATGTATGATCAAAAGAGGCTTACGTTTGTCTATCATCTTCAGTTCCAGAGCA	3000

QY	3001	ACGAAACGTGGA	CTACTTCTCCAAATTAACATGAGCTTTTCA	CAAAACCCATATGCTATAC	3061
Db	3001	ACGAAACGTGGA	CTACTTCTCCAAATTAACATGAGCTTTTCA	CAAAACCCATATGCTATAC	3061
QY	3061	CACCACTTTTT	CCGATCAAGTCATTTGGTTAAACCTAAATGTAAAGAAAATCTGCTAGAGG	3120	
Db	3061	CACCACTTTTT	CCGATCAAGTCATTTGGTTAAACCTAAATGTAAAGAAAATCTGCTAGAGG	3120	
QY	3121	AAAACCTTAGA	AAATCATTCACATGTCACCTGAAAGAAATGGGAAATAGAGAAACCTCCAA	3180	
Db	3121	AAAACCTTAGA	AAATCATTCACATGTCACCTGAAAGAAATGGGAAATAGAGAAACCTCCAA	3180	
QY	3181	GTACAGTGA	GCACATTAAGCCGTAAATACATTAGAGAAAATGTTTTTAAAGAGCAGCT	3240	
Db	3181	GTACAGTGA	GCACATTAAGCCGTAAATACATTAGAGAAAATGTTTTTAAAGAGCAGCT	3240	
QY	3241	CAAGCAATTTAA	TGAAGTAGTTCACGACTTAATGAAGTGCGCTCCAGTATTAATGA	3300	
Db	3241	CAAGCAATTTAA	TGAAGTAGTTCACGACTTAATGAAGTGCGCTCCAGTATTAATGA	3300	
QY	3301	TAGGTTCCAGT	ATGATAAATTCACAGAGAACTAGTAGAGAAACAGAGGGCCAAATATGA	3360	
Db	3301	TAGGTTCCAGT	ATGATAAATTCACAGAGAACTAGTAGAGAAACAGAGGGCCAAATATGA	3360	
QY	3361	ATGCTATGCTT	AGATTAGGGGTTTTGCACCTGAGGCTATATAAACAAAGTCTTCCTGAA	3420	
Db	3361	ATGCTATGCTT	AGATTAGGGGTTTTGCACCTGAGGCTATATAAACAAAGTCTTCCTGAA	3420	
QY	3421	GTAATTTGA	ACATTCCTGAAATTAACAAAGCAAGATATGAAGAGTAGTTCAGACCTGTA	3480	
Db	3421	GTAATTTGA	ACATTCCTGAAATTAACAAAGCAAGATATGAAGAGTAGTTCAGACCTGTA	3480	
QY	3481	ATACAGATTTCT	CCATATCTGATTTCCAGATTAACCTTAGAACACGCTATGGGAATGATC	3540	
Db	3481	ATACAGATTTCT	CCATATCTGATTTCCAGATTAACCTTAGAACACGCTATGGGAATGATC	3540	
QY	3541	ATGCATCTCAG	GGTTGTTCTGAGACACTGTATGACCTGTTAGATGATGCTGAATTAAGG	3600	
Db	3541	ATGCATCTCAG	GGTTGTTCTGAGACACTGTATGACCTGTTAGATGATGCTGAATTAAGG	3600	
QY	3601	AAGATPACT	AGTTTGGCTGAAATAATACATTAAGAAAGTTCGCTGTTTTTGACAAAGCG	3660	
Db	3601	AAGATPACT	AGTTTGGCTGAAATAATACATTAAGAAAGTTCGCTGTTTTTGACAAAGCG	3660	
QY	3661	TCCAGAAAG	GAGAGCTTAGCAGAGAGTCTTAGCCCTTCAACCATACACATTTGGCTCAGG	3720	
Db	3661	TCCAGAAAG	GAGAGCTTAGCAGAGAGTCTTAGCCCTTCAACCATACACATTTGGCTCAGG	3720	
QY	3721	GTTACCGA	AGAGGGGCCAAGAAATTAAGTCCCTAGAGAAAGAACTTATCTGTAGAGATG	3780	
Db	3721	GTTACCGA	AGAGGGGGCCAAAGAAATTAAGTCCCTAGAGAAAGAACTTATCTGTAGAGATG	3780	
QY	3781	AAGAGCTTCC	CGCTTCCAACTGTTATTTGGTTAAAGTAAACAATAATACCTTCTCAGT	3840	
Db	3781	AAGAGCTTCC	CGCTTCCAACTGTTATTTGGTTAAAGTAAACAATAATACCTTCTCAGT	3840	
QY	3841	CTACTAGG	CATAGCAGGTCCTACCGAGTGTCTGTCTTAAGACACACAGAGAGAAATTTAT	3900	
Db	3841	CTACTAGG	CATAGCAGGTCCTACCGAGTGTCTGTCTTAAGACACACAGAGAGAAATTTAT	3900	
QY	3901	TATCATTTGA	AGAAATAGCTTAAATGACAGAGTAAACCAAGTAAATTTGGCAAAAGGCACTC	3960	
Db	3901	TATCATTTGA	AGAAATAGCTTAAATGACAGAGTAAACCAAGTAAATTTGGCAAAAGGCACTC	3960	
QY	3961	AGGAACAT	CACTTAGTAGAGAAACAAATGTTCTGCTAGCTGGTTTTCTTCAACAGTGA	4020	
Db	3961	AGGAACAT	CACTTAGTAGAGAAACAAATGTTCTGCTAGCTGGTTTTCTTCAACAGTGA	4020	
QY	4021	GTGAATTG	GAAGACTTGAAGTCAATATACAAACACCCAGAGATCTTTCTTGATTTGGTCTT	4080	
Db	4021	GTGAATTG	GAAGACTTGAAGTCAATATACAAACACCCAGAGATCTTTCTTGATTTGGTCTT	4080	

QY	4081	CCAAACAAATAGGATCAGCTCTCTAACCCAGGGAGTTGCTGTGATACAAAGAAATTGG	4144
Db	4081	CCAAACAAATAGGATCAGCTCTCTAACCCAGGGAGTTGCTGTGATACAAAGAAATTGG	4144
QY	4141	TTTCAGATGATGAAGAAAGAGAAAGGGCTTGGAGAAATATATCAAGAGCAAAACA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAAGGGCTTGGAGAAATATATCAAGAGCAAAACA	4200
QY	4201	TGATATTCAACTTAGTGTAAGCAGCATCTGGGTGTGAAGTGAACAAGCCTCTCTGAAG	4266
Db	4201	TGATATTCAACTTAGTGTAAGCAGCATCTGGGTGTGAAGTGAACAAGCCTCTCTGAAG	4266
QY	4261	ACTGTCAGGGCTATCCCTCTCAGATGTACATTTTAAACATCCAGAGAGGATATACATGC	4322
Db	4261	ACTGTCAGGGCTATCCCTCTCAGATGTACATTTTAAACATCCAGAGAGGATATACATGC	4322
QY	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTAGAACCTGTGTAGAACAGC	4388
Db	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTAGAACCTGTGTAGAACAGC	4388
QY	4381	ATGGAGCCAGCCTTTCTAACAGCTACCCCTTCATATAGTGAATCTTTCTGCTTTGAGG	4440
Db	4381	ATGGAGCCAGCCTTTCTAACAGCTACCCCTTCATATAGTGAATCTTTCTGCTTTGAGG	4440
QY	4441	ACCTGCCAAATTCAGAACCAACATCAGAAAAAGCAGTATTAATCTTACAGAAABATA	4500
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QY	4501	GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAGGTCTG	4560
Db	4501	GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAGGTCTG	4560
QY	4561	CAGATAGTTCTTACAGTAAAAATAAGAACCCAGAGTGAAGAGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTTACAGTAAAAATAAGAACCCAGAGTGAAGAGTCAATCCCTCTTAAT	4620
QY	4621	GCCCATCTTTGATATAGTGTGTACATGACAGTTGCTCTGGGAGCTTTCAGAAATAAA	4680
Db	4621	GCCCATCTTTGATATAGTGTGTACATGACAGTTGCTCTGGGAGCTTTCAGAAATAAA	4680
QY	4681	ACTACCCATCTTCAAGAGAGCTCATTTAAGTTGTGATGTGGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTACCCATCTTCAAGAGAGCTCATTTAAGTTGTGATGTGGAGAGCAACAGCTGGAAG	4740
QY	4741	AGTCTGGGCCACAGCATTTGACGAAACATCTTACTTGTCCAAAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACAGCATTTGACGAAACATCTTACTTGTCCAAAGGCAAGATCTAGAGGAA	4800
QY	4801	CCCCCTACTGGAATCTGGAATCAGACCTCTTCTGTGATGACCCCTGAATCTGATCCTTCTG	4860
Db	4801	CCCCCTACTGGAATCTGGAATCAGACCTCTTCTGTGATGACCCCTGAATCTGATCCTTCTG	4860
QY	4861	AAGACAGAGCCCCCAGAGTCAAGCTCGTGTGGCAATACATCACTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGAGCCCCCAGAGTCAAGCTCGTGTGGCAATACATCACTTCAACCTCTGATTTGA	4920
QY	4921	AAGTTCCCAATTGAAGTTGACAGATCTGCCAGAGTCAAGCTCTGCTCATACTG	4980
Db	4921	AAGTTCCCAATTGAAGTTGACAGATCTGCCAGAGTCAAGCTCTGCTCATACTG	4980
QY	4981	ATATCGCTGGGTATTAATGCAATGGAAGAAAGTGTAGCAGGAGGAAGCCAGAAATTGAAG	5040
Db	4981	ATATCGCTGGGTATTAATGCAATGGAAGAAAGTGTAGCAGGAGGAAGCCAGAAATTGAAG	5040
QY	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGGTGGTCTGGCTGAGCCCAAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGGTGGTCTGGCTGAGCCCAAG	5100
QY	5101	AATTTATGCTGTGTACAAAGTTTGCCAGAAACACACATCACTTTAATCTATCTAATTA	5160
Db	5101	AATTTATGCTGTGTACAAAGTTTGCCAGAAACACACATCACTTTAATCTATCTAATTA	5160
QY	5161	CTGAAGAGACTACATGTTGTTATGAAGAACAGATGCTGAGTTGTGTGAACGAGAC	5220

Db	5161	CTGAAGACACTCACTCACTCTGTATGAAACACAGTCTGAAGTTGTGTGTAACGACAC	5220
Qy	5221	TGAAATATTTTCTAGAAATTCGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Db	5221	TGAATATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Qy	5281	AGCTATTTAAAGAAAGAAAAATGCTGAAATGACATGATTTTGAAGTCAGAGAGAAATGTGG	5340
Db	5281	AGCTATTTAAAGAAAGAAAAATGCTGAAATGACATGATTTTGAAGTCAGAGAGAAATGTGG	5340
Qy	5341	TCAATGGAAGAACCCACCAGGTCCAAAGCAGCAAGAGAAATCCCAGAGCAGAAAGATCT	5400
Db	5341	TCAATGGAAGAACCCACCAGGTCCAAAGCAGCAAGAGAAATCCCAGAGCAGAAAGATCT	5400
Qy	5401	TCAGGGGGCTTGAATCTGTTGCTATGAGGCCCTTACCAACATGCCACAGATCAACTGG	5460
Db	5401	TCAGGGGGCTTGAATCTGTTGCTATGAGGCCCTTACCAACATGCCACAGATCAACTGG	5460
Qy	5461	AATGATGATGTCACAGTGTGTGTCTTCTGTGTGGAAGAGCTTTCATTCATCCCTTG	5520
Db	5461	AATGATGATGTCACAGTGTGTGTCTTCTGTGTGGAAGAGCTTTCATTCATCCCTTG	5520
Qy	5521	GCACAGGTGTCCACCCCAATTTGGTGTGACGACAGATGCTGTGACAGAGACATGGCT	5580
Db	5521	GCACAGGTGTCCACCCCAATTTGGTGTGACGACAGATGCTGTGACAGAGACATGGCT	5580
Qy	5581	TCATGCAATTTGGGCGAGTGTGTAGGCACTGTGTGTGACCCGAGAGTGGGTGTGACA	5640
Db	5581	TCATGCAATTTGGGCGAGTGTGTAGGCACTGTGTGTGACCCGAGAGTGGGTGTGACA	5640
Qy	5641	GTTGAGCACTTACACAGTCCAGAGAGCTGGAACCTTACCTGATATCCCAATCCCCACA	5700
Db	5641	GTTGAGCACTTACACAGTCCAGAGAGCTGGAACCTTACCTGATATCCCAATCCCCACA	5700
Qy	5701	GCACACTACTGA 5711	
Db	5701	GCACACTACTGA 5711	

RESULT 2
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 Sequence 5, Application US/09982828
 Publication No. US20030022184A1
 GENERAL INFORMATION:
 APPLICANT: Murphy, Patricia D.
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 TITLE OF INVENTION: Coding Sequences of the Human
 BRCA1 Gene
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan Lewis & Bockius LLP
 STREET: 1111 Pennsylvania Avenue N. W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/598,591
FILING DATE: 1996-02-12
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL (om13)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-982-828-5

Query Match 100.0%; Score 5711; DB 9; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGTGAACCCGACAGGCTGTGGGTTTCTCAGATACTGGCC 60
DB 1 AGCTCGCTGAGACTTCTCGTGAACCCGACAGGCTGTGGGTTTCTCAGATACTGGCC 60
QY 61 CTTGCGCTGAGAGGCGCTTCACTCTGCTGTGGTAAAGTTCAATGGAAACAGAAAGAA 120
DB 61 CTTGCGCTGAGAGGCGCTTCACTCTGCTGTGGTAAAGTTCAATGGAAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTCGGCTTGAAGAATACAAATGCTATTATGCTATGCAAGAAA 180
DB 121 TGGATTATCTGCTCTTCGGCTTGAAGAATACAAATGCTATTATGCTATGCAAGAAA 180
QY 181 TCTTAAGTGTCCCATCTGCTGGAAGTGTATCAAGAACCTGCTCCACAAAGTGTACC 240
DB 181 TCTTAAGTGTCCCATCTGCTGGAAGTGTATCAAGAACCTGCTCCACAAAGTGTACC 240
QY 241 ACAATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT 300
DB 241 ACAATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT 300
QY 301 GTCTTTATGTATGAATGATATACCAAAAGAGGCTTCAAGAAAGTACAGATTTTATGTC 360
DB 301 GTCTTTATGTATGAATGATATACCAAAAGAGGCTTCAAGAAAGTACAGATTTTATGTC 360
QY 361 AACTTGTGAAGAGCTATTGAATCATTTTGTCTTTTGTGACAGAGGTTTGGAGT 420
DB 361 AACTTGTGAAGAGCTATTGAATCATTTTGTCTTTTGTGACAGAGGTTTGGAGT 420
QY 421 ATGCAAAACAGCTAATTTTGCAGAAAGAGAAATATCTCTCTGAACATCTTAAAGATG 480
DB 421 ATGCAAAACAGCTAATTTTGCAGAAAGAGAAATATCTCTCTGAACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCCCAAGATAGGCTACAGAAACCGTCCAAAGAACTTTTACAGATG 540
DB 481 AAGTTTCTATCATCCCAAGATAGGCTACAGAAACCGTCCAAAGAACTTTTACAGATG 540
QY 541 AACCCGAAATCTTCTCTTGCAGAAACAGCTCTCAAGTGTCAACTCTTAACTTGGAA 600
DB 541 AACCCGAAATCTTCTCTTGCAGAAACAGCTCTCAAGTGTCAACTCTTAACTTGGAA 600
QY 601 CTGTGAAACTGTAGAGACAAAGCAGGATACAACTTCAAAAGAGCTGTCTTACATTTG 660

DB 601 CTGTGAAACTGTAGAGACAAAGCAGGATACAACTTCAAAAGAGCTGTCTTACATTTG 660
QY 661 AATTGGATCTGATTTCTTCTGAAAGATACGTTAATAGGCAATTTATGCAAGTGGAG 720
DB 661 AATTGGATCTGATTTCTTCTGAAAGATACGTTAATAGGCAATTTATGCAAGTGGAG 720
QY 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGAAACAGAGATGAATCAGTTTGGATTTG 780
DB 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGAAACAGAGATGAATCAGTTTGGATTTG 780
QY 781 CAAAAAAGCTGCTGTGATTTTCTGAGACGATTTAACAATATCTGAACATCATCAC 840
DB 781 CAAAAAAGCTGCTGTGATTTTCTGAGACGATTTAACAATATCTGAACATCATCAC 840
QY 841 CCAGTAATATATGTTTGAACACACAGAGAGGCTGACAGGATCCGAGAAAGT 900
DB 841 CCAGTAATATATGTTTGAACACACAGAGAGGCTGACAGGATCCGAGAAAGT 900
QY 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGACCATGTGGACAAATATCTCATGCCA 960
DB 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGACCATGTGGACAAATATCTCATGCCA 960
QY 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTCACTAAGACAGATGATGTAGAAA 1020
DB 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTCACTAAGACAGATGATGTAGAAA 1020
QY 1021 AGGCTGAATTCGTGTAATTAAGCAACAGCTGGCTTACAGAGGCCCAATCAAGAT 1080
DB 1021 AGGCTGAATTCGTGTAATTAAGCAACAGCTGGCTTACAGAGGCCCAATCAAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGATGAAATAGCAAGAACTGCTATGCT 1200
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGATGAAATAGCAAGAACTGCTATGCT 1200
QY 1201 CAGAGATCTTGAAGATGATGAAAGTCTTGTGATACATTAATACAGATTCACA 1260
DB 1201 CAGAGATCTTGAAGATGATGAAAGTCTTGTGATACATTAATACAGATTCACA 1260
QY 1261 AAGTTATGAGTGTGTTTCCAGAAAGTATGAACTGTTAGGTTCTGATGACTCATGATG 1320
DB 1261 AAGTTATGAGTGTGTTTCCAGAAAGTATGAACTGTTAGGTTCTGATGACTCATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATGTGACGTTCTAATGAGGTAGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGTGTATGTGACGTTCTAATGAGGTAGATG 1380
QY 1381 AATATTTCTGTTCTTCAAGAAATAGACTTACTGCGCAGTATCTCATAGAGCTTTAA 1440
DB 1381 AATATTTCTGTTCTTCAAGAAATAGACTTACTGCGCAGTATCTCATAGAGCTTTAA 1440
QY 1441 TATGTAAAGTAAAGAGTCTCAATCAAGTATGAGATATATTAAGCAAAATAT 1500
DB 1441 TATGTAAAGTAAAGAGTCTCAATCAAGTATGAGATATATTAAGCAAAATAT 1500
QY 1501 TTGGGAAACCTATGGAAGAGGCAAGGCTCCCAACTTAAGCATGTAACTGAAATTC 1560
DB 1501 TTGGGAAACCTATGGAAGAGGCAAGGCTCCCAACTTAAGCATGTAACTGAAATTC 1560
QY 1561 TAAATATGAGACATTTGTTACTGAGCCACATATATACAAAGGCTCCCTCACAAATA 1620
DB 1561 TAAATATGAGACATTTGTTACTGAGCCACATATATACAAAGGCTCCCTCACAAATA 1620
QY 1621 AATTAAAGGCTAAAGAGACCTATACAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
DB 1621 AATTAAAGGCTAAAGAGACCTATACAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGAGTTCAAAAGACTCTGTAATGATTAATCAGGAACTAACCAAGGAGC 1740

D	b	1681	CAGATTTGGCAGCTTCAAAAAGACTCTGGAAATGATTAATACAGGAACTAACCAAAACGAGAC	1744
Q	y	1741	AGAATGCTCAAGTGAATATTAATTAATAGTGTGATGAGATTAACAAAGGTGATT	1800
D	b	1741	AGAAATGGCTCAAGTGAATATTAATTAATAGTGTGATGAGATTAACAAAGGTGATT	1800
Q	y	1801	CTATTACAAATGAGAAAATCCTAACCCAAATGAAATCACTGGAAAAGAAATCTGGTTCA	1866
D	b	1801	CTATTACAAATGAGAAAATCCTAACCCAAATGAAATCACTGGAAAAGAAATCTGGTTCA	1866
Q	y	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAACTCCAAATTAATATCC	1920
D	b	1861	AAACGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAACTCCAAATTAATATCC	1920
Q	y	1921	ACAAATTCAAAAGCACCCTAAGAAATAGCTGAGGAGAGTCTTCTACAGCATATTC	1980
D	b	1921	ACAAATTCAAAAGCACCCTAAGAAATAGCTGAGGAGAGTCTTCTACAGCATATTC	1980
Q	y	1981	ATGCGCTTGAATAGTACTAGTAGAAATCTAAGCCCATTAATTTGTACTGAATTGGCAA	2040
D	b	1981	ATGCGCTTGAATAGTACTAGTAGAAATCTAAGCCCATTAATTTGTACTGAATTGGCAA	2040
Q	y	2041	TTGATAGTTGTTCTAAGCGTGAAGAGATTAAGAAAAAAAAGTACAAACAAATTCGACATCA	2100
D	b	2041	TTGATAGTTGTTCTAAGCGTGAAGAGATTAAGAAAAAAAAGTACAAACAAATTCGACATCA	2100
Q	y	2101	GGCACAGCAGAAAACCTACAACTCAAGAAAGTTAAAGAACTTGCACTGAGACCAAGAA	2160
D	b	2101	GGCACAGCAGAAAACCTACAACTCAAGAAAGTTAAAGAACTTGCACTGAGACCAAGAA	2160
Q	y	2161	GTAACAGCCCAATATACAGACAGTAAAGACATGACAGCGATCTTTCCAGAGCTGA	2220
D	b	2161	GTAACAGCCCAATATACAGACAGTAAAGACATGACAGCGATCTTTCCAGAGCTGA	2220
Q	y	2221	AGTTAACAAATGACACTGGTCTTTTCTAAGTGTCTAAATACAGCTGAACCTTAAGAAAT	2280
D	b	2221	AGTTAACAAATGACACTGGTCTTTTCTAAGTGTCTAAATACAGCTGAACCTTAAGAAAT	2280
Q	y	2281	TTGTCAATCTCAGCCTTCCAAAGAGAAAGAAAGAGAAACCTAAGAAACAGTTAAAGTGT	2340
D	b	2281	TTGTCAATCTCAGCCTTCCAAAGAGAAAGAAAGAGAAACCTAAGAAACAGTTAAAGTGT	2340
Q	y	2341	CTAATTAATGCTGAGAAACCCCAAAAGTCTCATGTTTAAGTGGAGAAAGGTTTGGCAAATG	2400
D	b	2341	CTAATTAATGCTGAGAAACCCCAAAAGTCTCATGTTTAAGTGGAGAAAGGTTTGGCAAATG	2400
Q	y	2401	AAAGATCTGTGAGAGTGAAGCTATTTCAATGGTGAACCTGATCTGATTAATGAGCACTCAG	2460
D	b	2401	AAAGATCTGTGAGAGTGAAGCTATTTCAATGGTGAACCTGATCTGATTAATGAGCACTCAG	2460
Q	y	2461	AAAGATCTGTGAGAGTGAAGCTATTTCAATGGTGAACCTGATCTGATTAATGAGCACTCAG	2520
D	b	2461	AAAGATCTGTGAGAGTGAAGCTATTTCAATGGTGAACCTGATCTGATTAATGAGCACTCAG	2520
Q	y	2521	GTGTGAGTCAGTGTGACAGATTTGAAACCCCAAGAGGACTAAATTCATGAGTGTTCCAAAG	2580
D	b	2521	GTGTGAGTCAGTGTGACAGATTTGAAACCCCAAGAGGACTAAATTCATGAGTGTTCCAAAG	2580
Q	y	2581	ATAATATGAAATGACACAGAAAGCTTAAAGTATCCATTTGGGACATGAAGTTAACCACTG	2640
D	b	2581	ATAATATGAAATGACACAGAAAGCTTAAAGTATCCATTTGGGACATGAAGTTAACCACTG	2640
Q	y	2641	GGGAAACCAAGCACTAAGAAATGAGAAAGTGAACCTTATGATGCTCAGATTTTGGCAATACAT	2700
D	b	2641	GGGAAACCAAGCACTAAGAAATGAGAAAGTGAACCTTATGATGCTCAGATTTTGGCAATACAT	2700
Q	y	2701	TCAAGGTTTCAAAAGGCCAGCTATTTGCTGTGTTTCAAAATCCAGAAATGACAGAAAGG	2760
D	b	2701	TCAAGGTTTCAAAAGGCCAGCTATTTGCTGTGTTTCAAAATCCAGAAATGACAGAAAGG	2760
Q	y	2761	AATGTGCAACATTTCTCTGCCCCTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
D	b	2761	AATGTGCAACATTTCTCTGCCCCTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT	2820

OY	2821	TTGAAATGTGAA	CAAA	AAGAAAGAAA	ATCA	AGAAAGAA	TAGTGTCT	TAATATCA	ATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAA	CAAA	AAGAAAGAAA	ATCA	AGAAAGAA	TAGTGTCT	TAATATCA	ATCAAGCTGTAC	2880
OY	2881	AGACAGTTAA	TATCACTG	CAGGCTTCTCTG	TGTGTG	GTCA	GAAGAA	GATTAAGC	ATTGATATA	2940
Db	2881	AGACAGTTAA	TATCACTG	CAGGCTTCTCTG	TGTGTG	GTCA	GAAGAA	GATTAAGC	ATTGATATA	2940
OY	2941	ATGCCAAATGT	ATATCA	TAAGAGAGGCTCT	TAGGTTTGTCT	ATCATCT	TCAGTTCA	GAGGCA	3000	
Db	2941	ATGCCAAATGT	ATATCA	TAAGAGAGGCTCT	TAGGTTTGTCT	ATCATCT	TCAGTTCA	GAGGCA	3000	
OY	3001	ACGAAAC	TCGAGCTCA	TACTACTCCAA	TATAAACATG	SACCTTTT	TACA	CAAAACCCATATG	CTGTATAC	3060
Db	3001	ACGAAAC	TCGAGCTCA	TACTACTCCAA	TATAAACATG	SACCTTTT	TACA	CAAAACCCATATG	CTGTATAC	3060
OY	3061	CACCACTTTT	CCCATCA	AGTCAATTTG	TTTAAACCTTAA	TATAGAAAAAT	CTGCTAGAGC	3120		
Db	3061	CACCACTTTT	CCCATCA	AGTCAATTTG	TTTAAACCTTAA	TATAGAAAAAT	CTGCTAGAGC	3120		
OY	3121	AAAACCTTTG	AGGAACAT	TTCAATGTCA	CTGTAAGAAATGGG	AAATGAGAAC	CTTCCAA	3180		
Db	3121	AAAACCTTTG	AGGAACAT	TTCAATGTCA	CTGTAAGAAATGGG	AAATGAGAAC	CTTCCAA	3180		
OY	3181	GTACAGTGAG	CACATTA	TAGCCGTAT	ATACATTA	TAGAAAAATG	TTTTTAAAGAAC	CACAGCT	3240	
Db	3181	GTACAGTGAG	CACATTA	TAGCCGTAT	ATACATTA	TAGAAAAATG	TTTTTAAAGAAC	CACAGCT	3240	
OY	3241	CAAGCAATAT	TATTAATGA	AGTAGGCTTCC	CAGTACTATGA	AGTGGGCTCC	CAGTATTA	TATGAA	3300	
Db	3241	CAAGCAATAT	TATTAATGA	AGTAGGCTTCC	CAGTACTATGA	AGTGGGCTCC	CAGTATTA	TATGAA	3300	
OY	3301	TAGGTTCC	AGGATGAA	AAAAACAT	TCAACAGAACTAG	GTAGAAACAG	AGGGCCAA	AAATATGA	3360	
Db	3301	TAGGTTCC	AGGATGAA	AAAAACAT	TCAACAGAACTAG	GTAGAAACAG	AGGGCCAA	AAATATGA	3360	
OY	3361	ATGCTATGCT	TAGATTAG	GGGGTTTTG	CAACCTGAGG	CTATTA	AAACAAAGTCTT	CTTGGA	3420	
Db	3361	ATGCTATGCT	TAGATTAG	GGGGTTTTG	CAACCTGAGG	CTATTA	AAACAAAGTCTT	CTTGGA	3420	
OY	3421	GTAATTTGA	ACATCC	CGAAATTA	AAAAAGCAGAA	TATGAA	AGAGTGGT	CAGACTGTA	3480	
Db	3421	GTAATTTGA	ACATCC	CGAAATTA	AAAAAGCAGAA	TATGAA	AGAGTGGT	CAGACTGTA	3480	
OY	3481	ATACAGATTT	CTCTCA	TATCTGATTT	CAGATTA	CTTAGAAC	CAGCCTTA	TGGGAATGATC	3540	
Db	3481	ATACAGATTT	CTCTCA	TATCTGATTT	CAGATTA	CTTAGAAC	CAGCCTTA	TGGGAATGATC	3540	
OY	3541	ATGCATCT	CAGGTTTGT	TTCTGAGACACT	GTATGACCTG	TAGATGAT	AGATGGTGA	ATTAAGG	3600	
Db	3541	ATGCATCT	CAGGTTTGT	TTCTGAGACACT	GTATGACCTG	TAGATGAT	AGATGGTGA	ATTAAGG	3600	
OY	3601	AAGATTA	CTAGTTTGT	CTGAAAAATACAT	TAAAGAAATTT	CTGCTG	TTTTTAA	AGCAAAACG	3660	
Db	3601	AAGATTA	CTAGTTTGT	CTGAAAAATACAT	TAAAGAAATTT	CTGCTG	TTTTTAA	AGCAAAACG	3660	
OY	3661	TCCAGAAA	AGAGAGCT	TAGCAGAGAGT	CTTAAGCCCTT	TACCCAT	ATACATTTGG	CTCAGG	3720	
Db	3661	TCCAGAAA	AGAGAGCT	TAGCAGAGAGT	CTTAAGCCCTT	TACCCAT	ATACATTTGG	CTCAGG	3720	
OY	3721	GTTACCGA	AGAGGGGCCA	AGAAATTA	TAGAGTCT	CAGAAAGAACTT	ATCTAGT	AGAGTG	3780	
Db	3721	GTTACCGA	AGAGGGGCCA	AGAAATTA	TAGAGTCT	CAGAAAGAACTT	ATCTAGT	AGAGTG	3780	
OY	3781	AAGAGCTT	CCCTGCTT	CCAACTTTG	TATTTGGT	TAAAGTAA	CAATATAC	CTTCTCAGT	3840	
Db	3781	AAGAGCTT	CCCTGCTT	CCAACTTTG	TATTTGGT	TAAAGTAA	CAATATAC	CTTCTCAGT	3840	
OY	3841	CTACTAG	GCATAG	CACGCTGTCT	ACGAGTGTCTGT	CTTA	AGAACACAG	AGAGAAATTTAT	3900	
Db	3841	CTACTAG	GCATAG	CACGCTGTCT	ACGAGTGTCTGT	CTTA	AGAACACAG	AGAGAAATTTAT	3900	

QY 3901 TATCATGGAAGTAAGTAAATGACTGACGTAAACAGGTAATATTGGCAAGGCAATCTC 3960
 Db 3901 TATCATGGAAGTAAGTAAATGACTGACGTAAACAGGTAATATTGGCAAGGCAATCTC 3960
 QY 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
 Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
 QY 4021 GTGAATTGGAAGACTGACGAAATACAAACACCCAGATCCCTTTGATGTTGTTCTT 4080
 Db 4021 GTGAATTGGAAGACTGACGAAATACAAACACCCAGATCCCTTTGATGTTGTTCTT 4080
 QY 4081 CCAAAACAATGAGGCACTGCTGAAACCCAGGAGTTGTTCTGAGTACAGAAATGG 4140
 Db 4081 CCAAAACAATGAGGCACTGCTGAAACCCAGGAGTTGTTCTGAGTACAGAAATGG 4140
 QY 4141 TTTTCAAGTATGAAAGAAAGGAAACGGGCTTGGAAAGAAATTAATCAAGAAAGCA 4200
 Db 4141 TTTTCAAGTATGAAAGAAAGGAAACGGGCTTGGAAAGAAATTAATCAAGAAAGCA 4200
 QY 4201 TGAATTCAACTTAGTGAAGCAGCATCTGGGTGTGAGTGAACAAAGGCTCTGAG 4260
 Db 4201 TGAATTCAACTTAGTGAAGCAGCATCTGGGTGTGAGTGAACAAAGGCTCTGAG 4260
 QY 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGAGATACATGC 4320
 Db 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGAGATACATGC 4320
 QY 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATGAAGCTGTGTGAACAGC 4380
 Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATGAAGCTGTGTGAACAGC 4380
 QY 4381 ATGGAGGCGAGCCTTCTCAAGCTACCTTCCATCAATGAGTGAATCTTCTGAG 4440
 Db 4381 ATGGAGGCGAGCCTTCTCAAGCTACCTTCCATCAATGAGTGAATCTTCTGAG 4440
 QY 4441 ACCTCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACTTCAAGAAAAAT 4500
 Db 4441 ACCTCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACTTCAAGAAAAAT 4500
 QY 4501 GTGAATACCTTATTAAGCAGAAATCCAGAGGCTTTTCTGCTGACAGTTGAGTGTCTG 4560
 Db 4501 GTGAATACCTTATTAAGCAGAAATCCAGAGGCTTTTCTGCTGACAGTTGAGTGTCTG 4560
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 Db 4561 CAGATGTTTACACAGTAAATTAAGAACCCAGAGTGAAGAGTCAATCCCTTTCTAAT 4620
 QY 4621 GCCCATCATTAAGTATGAGTGTGATGACAGTGTCTCTGAGAGTCTTCAAGATGA 4680
 Db 4621 GCCCATCATTAAGTATGAGTGTGATGACAGTGTCTCTGAGAGTCTTCAAGATGA 4680
 QY 4681 ACTAACCATTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGAG 4740
 Db 4681 ACTAACCATTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGAG 4740
 QY 4741 AGTGTGGGCAACGATTTGACGGAACATCTTACTTGGCAAGCAAGCTGAGAGG 4800
 Db 4741 AGTGTGGGCAACGATTTGACGGAACATCTTACTTGGCAAGCAAGCTGAGAGG 4800
 QY 4801 CCCCTTACCTGATCTGAATCAGCTCTTCTCTGATGACCTGATCTGATCTTCTG 4860
 Db 4801 CCCCTTACCTGATCTGAATCAGCTCTTCTCTGATGACCTGATCTGATCTTCTG 4860
 QY 4861 AAGACAGAGCCCAAGAGTCAAGCTGTGTGTGCAACATCACTTCAAGCTGCAATGA 4920
 Db 4861 AAGACAGAGCCCAAGAGTCAAGCTGTGTGTGCAACATCACTTCAAGCTGCAATGA 4920
 QY 4921 AAGTGTCCCAATGAAGTGTGCAAGATCTCCAGAGTCCAGTGTGCTCAATCACTG 4980
 Db 4921 AAGTGTCCCAATGAAGTGTGCAAGATCTCCAGAGTCCAGTGTGCTCAATCACTG 4980
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Db 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTGACAGGAGAGAGCCAGAAATTGACAG 5040
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 Db 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTGCTGACCCCAAG 5100
 QY 5101 AATTATGCTCGTCAAGTGTGACAGAAACACCAACATCACTTAATTAATTA 5160
 Db 5101 AATTATGCTCGTCAAGTGTGACAGAAACACCAACATCACTTAATTAATTA 5160
 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATCTGAGTTGTGTGAACGAC 5220
 Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATCTGAGTTGTGTGAACGAC 5220
 QY 5221 TGAATATTTTCTAGGAATTTGGGGAGGAAATGGGTAGTGTGCTTTCTGGGTGACC 5280
 Db 5221 TGAATATTTTCTAGGAATTTGGGGAGGAAATGGGTAGTGTGCTTTCTGGGTGACC 5280
 QY 5281 AGTCTATTAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGAGATGTG 5340
 Db 5281 AGTCTATTAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGAGATGTG 5340
 QY 5341 TCAATGAAAGAAACCAAGAGTCCAAAGCAGAAAGAAATCCAGACAGAAAGTCT 5400
 Db 5341 TCAATGAAAGAAACCAAGAGTCCAAAGCAGAAAGAAATCCAGACAGAAAGTCT 5400
 QY 5401 TCAGGGGGCTAGAAATCTGTGTATGGGCTTCAACCAACATGCCACAGATCACTG 5460
 Db 5401 TCAGGGGGCTAGAAATCTGTGTATGGGCTTCAACCAACATGCCACAGATCACTG 5460
 QY 5461 AATGATGTGACAGCTGTGTGCTTCTGTGTGAAGAGCTTTCATCACTTCACTG 5520
 Db 5461 AATGATGTGACAGCTGTGTGCTTCTGTGTGAAGAGCTTTCATCACTTCACTG 5520
 QY 5521 GCAAGAGTGTCAACCCCAATTTGTTGTGACAGCAGATCCTGACAGAGCAATGCT 5580
 Db 5521 GCAAGAGTGTCAACCCCAATTTGTTGTGACAGCAGATCCTGACAGAGCAATGCT 5580
 QY 5581 TCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGTGTGACA 5640
 Db 5581 TCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGTGTGACA 5640
 QY 5641 GTGTACACTCTACAGCTGTCAGAGAGCTGGAACCTAAGCTGATACCCAGATCCCA 5700
 Db 5641 GTGTACACTCTACAGCTGTCAGAGAGCTGGAACCTAAGCTGATACCCAGATCCCA 5700
 QY 5701 GCCACTACTGA 5711
 Db 5701 GCCACTACTGA 5711

RESULT 3

US-09-734-672-5
 ; Sequence 5, Application US/09734672
 ; Publication No. US20020183268A1

GENERAL INFORMATION:

APPLICANT: Murphy, Patricia D.
 ; Allen, Antonette C.
 ; Alvarez, Christopher P.
 ; Critz, Brenda S.
 ; Olson, Sheri J.
 ; Schelter, Denise B.
 ; Zeng, Bin
 TITLE OF INVENTION: Coding Sequences of the Human
 ; BRCA1 Gene
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan Lewis & Bockius LLP
 ; STREET: 1111 Pennsylvania Ave., N.W.
 ; CITY: Washington
 ; STATE: District of Columbia
 ; COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,672
FILING DATE: 03-Dec-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/966,436
FILING DATE: 07-No. US20020183268A1-97
APPLICATION NUMBER: US 08/598,591
FILING DATE: 12-Feb-96
ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tucson
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44921-5055-02-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20020183268A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-734-672-5
Query Match: 99.9%; Score 5703; DB 9; Length 5711;
Best Local Similarity: 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCTCGTGAAGATTCTGAGACCCGACACAGGCTGTGGGGTTCTCAGATTAAGTGGCC 60
DB 1 AGCTCGTGAAGATTCTGAGACCCGACACAGGCTGTGGGGTTCTCAGATTAAGTGGCC 60
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DB 61 CCGCGCTCAGAGAGGCTTCAACCTCTGCTCTGGTTAAAGTTGTTGAAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTGCGTTGAAAGTACAAAGTCAATTAAGCTATGACAGAA 180
DB 121 TGGATTATCTGCTCTGCGTTGAAAGTACAAAGTCAATTAAGCTATGACAGAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC 240
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC 240
QY 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACGAGAAAGGCGCTTCACAGT 300
DB 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACGAGAAAGGCGCTTCACAGT 300
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DB 301 GTCCCTTTATGTAAAGATGATTAACCAAGAGAGGCTTACAGAAAGTACAGAGTTAGTC 360
QY 361 AACTGTGTGAAGAGCTATTAAGAAATCATTTGTGCTTTTGAAGTTGAGTTGAGT 420
DB 361 AACTGTGTGAAGAGCTATTAAGAAATCATTTGTGCTTTTGAAGTTGAGTTGAGT 420
QY 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAGAAATTAAGTCTCTGAAACATCTTAAAGATG 480
DB 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAGAAATTAAGTCTCTGAAACATCTTAAAGATG 480

QY 481 AGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTTTACAGAGTG 540
DB 481 AGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTTTACAGAGTG 540
QY 541 AACCCGAAATCTCTTCTTGAAGAAACCAAGTCTGAGTTCCTCACTCTTAACCTTGGA 600
DB 541 AACCCGAAATCTCTTCTTGAAGAAACCAAGTCTGAGTTCCTCACTCTTAACCTTGGA 600
QY 601 CTGTAGAACTCTGAGCAAGAGGCGGATACAAACCTCAAAAGAGCTGTCTACACTTG 660
DB 601 CTGTAGAACTCTGAGCAAGAGGCGGATACAAACCTCAAAAGAGCTGTCTACACTTG 660
QY 661 AATTGGAGTCTGATCTTCTGAGATACCGTTAAAGCAACTTATTTGACAGTGGAG 720
DB 661 AATTGGAGTCTGATCTTCTGAGATACCGTTAAAGCAACTTATTTGACAGTGGAG 720
QY 721 ATCAAGAAATTTGTAACAAATCAACCCCTCAAGAACCGAGGATGAATCATGTTGATCTG 780
DB 721 ATCAAGAAATTTGTAACAAATCAACCCCTCAAGAACCGAGGATGAATCATGTTGATCTG 780
QY 781 CAAAAGAGCTGCTGTAATTTTCTGAGAGGATGTAACTGAATTAAGTACATCATCAAC 840
DB 781 CAAAAGAGCTGCTGTAATTTTCTGAGAGGATGTAACTGAATTAAGTACATCATCAAC 840
QY 841 CCAGTAATTAATGATTTGAAACAACCTGAGAGCGTGCAGCTGAGAGGCTCAGAAAAAT 900
DB 841 CCAGTAATTAATGATTTGAAACAACCTGAGAGCGTGCAGCTGAGAGGCTCAGAAAAAT 900
QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGAGGACCATGTGGCAAAATCTCATGCCA 960
DB 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGAGGACCATGTGGCAAAATCTCATGCCA 960
QY 961 GCTCATTTACAGATAGAGAACGAGTTTATTAACACATTAAGACAGATGATGAGAA 1020
DB 961 GCTCATTTACAGATAGAGAACGAGTTTATTAACACATTAAGACAGATGATGAGAA 1020
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTGAAGAGGCAACATTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTGAAGAGGCAACATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCAGACAAGAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCAGACAAGAAAAAGGTAG 1140
QY 1141 ATCTGAATTCGATATCCCTGTGTGAGAGAAAGAAATGGAATGAGCAAAATGCGATGCT 1200
DB 1141 ATCTGAATTCGATATCCCTGTGTGAGAGAAAGAAATGGAATGAGCAAAATGCGATGCT 1200
QY 1201 CAGAGATCTAGAGATCTGAGATGTTCTTGGATTAACATAATTAAGCAGATTGAGA 1260
DB 1201 CAGAGATCTAGAGATCTGAGATGTTCTTGGATTAACATAATTAAGCAGATTGAGA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTTATAGTTCTGATGATCAATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTTATAGTTCTGATGATCAATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTGTATTGAGAGCTTCTAAATGAGTGAATG 1380
DB 1321 GGGAGTCTGAATCAAAATCCAAAGTAGTGTATTGAGAGCTTCTAAATGAGTGAATG 1380
QY 1381 AATATTCGTGTTCTTCAAGAGAAATAGACTTACTGCGCAGTATCTCATAGGCTTTAA 1440
DB 1381 AATATTCGTGTTCTTCAAGAGAAATAGACTTACTGCGCAGTATCTCATAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTTCACTCAAAATGATGAGAGTAAATTAATTAAGACAAATAT 1500
DB 1441 TATGTAAAGTGAAGAGTTCACTCAAAATGATGAGAGTAAATTAATTAAGACAAATAT 1500
QY 1501 TTGGGAAATCCTATGAGAAAGAGCAAGCCTCCCACTTAAGCAGTAACTGAATATC 1560
DB 1501 TTGGGAAATCCTATGAGAAAGAGCAAGCCTCCCACTTAAGCAGTAACTGAATATC 1560
QY 1561 TAATTATAGAGCATTTGTTACTGAGCAGATTAATTAAGAGCGTCCCTCAAAATA 1620

1561 TAATTATAGAGAGCTTTGTACTGAGCCACAGATAATTAACAAGCCGCTCCCTCACAATA 1620
1621 AATTAAAGCTTAAAGAGAGACCTACATCAGACCTTCTCTGAGATTTTATCAAGAAG 1680
1621 AATTAAAGCTTAAAGAGAGACCTACATCAGACCTTCTCTGAGATTTTATCAAGAAG 1680
1681 CAGATTTGSCAGATTCAAAAGACTCTCTGAAATGATTAATCAGGAACTTACCAACGAGC 1740
1681 CAGATTTGSCAGATTCAAAAGACTCTCTGAAATGATTAATCAGGAACTTACCAACGAGC 1740
1741 AGAATGCTCAAGTGAATTAATTAATTAATGATGCTGATGGAATTAACAAAGGTCATT 1800
1741 AGAATGCTCAAGTGAATTAATTAATTAATGATGCTGATGGAATTAACAAAGGTCATT 1800
1801 CTATTGCAATGAGAAATCTCTAACCCATATGATCCTGCAAAAAGATCTGCTTCA 1860
1801 CTATTGCAATGAGAAATCTCTAACCCATATGATCCTGCAAAAAGATCTGCTTCA 1860
1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTCGAATTAATATCC 1920
1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTCGAATTAATATCC 1920
1921 ACAATTCAAAAGCACTTAAAGAAATGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
1921 ACAATTCAAAAGCACTTAAAGAAATGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
1981 ATGCGCTTGAAGTATGATGATGAGAAATTAAGCCACCTAATTTGATGATTTGCAAA 2040
1981 ATGCGCTTGAAGTATGATGATGAGAAATTAAGCCACCTAATTTGATGATTTGCAAA 2040
2041 TTGATAGTTGTTTGTAGCAGTGAAGATTAAGAAAGAAAGAAAGTAAACCAATCCAGTCA 2100
2041 TTGATAGTTGTTTGTAGCAGTGAAGATTAAGAAAGAAAGAAAGTAAACCAATCCAGTCA 2100
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2101 GGCACAGCAGAAACCTTCAACTCATGAGAGTTAAAGAACTGCAACTGAGCCAAAGGA 2160
2161 GTTAAAGCCAAATGAAAGACAAAGTAAAGAAATGATGAGAGCACTGCTTCCAGAGCTGA 2220
2161 GTTAAAGCCAAATGAAAGACAAAGTAAAGAAATGATGAGAGCACTGCTTCCAGAGCTGA 2220
2221 AGTTAAACAATGCACTGCTGTTCTTTTACTAAGTTCATAATACAGTGAATTAAGAAAT 2280
2221 AGTTAAACAATGCACTGCTGTTCTTTTACTAAGTTCATAATACAGTGAATTAAGAAAT 2280
2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGT 2340
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACG 2400
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACG 2400
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2461 AAAGATCTGAGAGATGAGATTAATTTGATGCTGATGATGATTAATGAGCACTCAGG 2520
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2581 AATAATGAATGACACAGAAAGCTTTAAGTATCATTTGGGACATGAGTTAAACACAGTC 2640
2581 AATAATGAATGACACAGAAAGCTTTAAGTATCATTTGGGACATGAGTTAAACACAGTC 2640
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2641 GGGAAACAAAGCATGAAATGGAAGAAAGTGAATTTATGCTCATTTTGGCAATATCAT 2700
2701 TCAAGGTTTCAAGGCCCAATGCTTGTCTGTTTCAATCCAGAAATGCAAGAGG 2760
2701 TCAAGGTTTCAAGGCCCAATGCTTGTCTGTTTCAATCCAGAAATGCAAGAGG 2760
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3301 TAGGTTCCAGTATGAAACATTTCAAGCAGAACTGATGAAACAGAGGCCAAATTTGA 3360
3361 ATGCTATGCTTGAATTTAGGAGGTTTGGCACTGAGGCTTAATAACAAATCTTCTGGA 3420
3361 ATGCTATGCTTGAATTTAGGAGGTTTGGCACTGAGGCTTAATAACAAATCTTCTGGA 3420
3421 GTTAATTTGATGATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTGAAGTGAAGTGA 3480
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3481 ATACAGATTTCTCTCAATATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 3540
3481 ATACAGATTTCTCTCAATATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 3540
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3601 AAGATATCTGAGGTTTGTCTGAGACCTGATGAGCTGTTAGATGATGATGATGATGAT 3660
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3661 TCCAGAAAGAGAGCTTGAAGAGAGCTTGAAGAGAGCTTGAAGAGAGCTTGAAGAGAG 3720
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3721 GTTACCGAAGAGGAGGCTCAAGAAATTAAGTCTCAGAAAGAGAACTTATCTAGAGATG 3780

QY 3781 AAGAGCTCCGCTTCCACACTTGTATTGTAAATTAACATATACCTTCAGT 3840
 Db 3781 AAGAGCTCCGCTTCCACACTTGTATTGTAAATTAACATATACCTTCAGT 3840
 QY 3841 CTACTAGGACATAGACCCGTTGCTACGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900
 Db 3841 CTACTAGGACATAGACCCGTTGCTACGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900
 QY 3901 TATCATTTGAAGATAGCTTAATATGACTGACATACAGGTATATTTGGCAAGGATCTTC 3960
 Db 3901 TATCATTTGAAGATAGCTTAATATGACTGACATACAGGTATATTTGGCAAGGATCTTC 3960
 QY 3961 AGGAACATACCTTGTGAGGAAACAAATGTCTGCTAGCTTTGTTTCTTCAACATGCA 4020
 Db 3961 AGGAACATACCTTGTGAGGAAACAAATGTCTGCTAGCTTTGTTTCTTCAACATGCA 4020
 QY 4021 GTGAATTTGGAAGACTTGAATGCAAAATACAAACCCAGGATCCTTCTTGATTGTTCTT 4080
 Db 4021 GTGAATTTGGAAGACTTGAATGCAAAATACAAACCCAGGATCCTTCTTGATTGTTCTT 4080
 QY 4081 CCAACCAATGAGGACATCAGTTGAAAGCCAGGAGTTGCTGAGTGAACAGGAATTTGG 4140
 Db 4081 CCAACCAATGAGGACATCAGTTGAAAGCCAGGAGTTGCTGAGTGAACAGGAATTTGG 4140
 QY 4141 TTTGAGATGATGAAGAAAGAGAACGGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200
 Db 4141 TTTGAGATGATGAAGAAAGAGAACGGGCTTGGAAAGAAATATCAAGAAAGCAAGCA 4200
 QY 4201 TGGATTTCAAACTTAGTGAGAGGACATCTGGGTGTGAGAGTGAACAGAGCTCTGAA 4260
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 QY 4321 AACATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAATGAAGAGTGTGTTGAACAG 4380
 Db 4321 AACATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAATGAAGAGTGTGTTGAACAG 4380
 QY 4381 ATGGAGGACGCTTCTTAACAGCTACCTTCCATCAATAGTACTTCTTGCCCTTGAG 4440
 Db 4381 ATGGAGGACGCTTCTTAACAGCTACCTTCCATCAATAGTACTTCTTGCCCTTGAG 4440
 QY 4441 ACCTGCGAATCCAGAACCAAGCAATCAAGAAAGCAAGTATTAACCTTCAAGAAAGTA 4500
 Db 4441 ACCTGCGAATCCAGAACCAAGCAATCAAGAAAGCAAGTATTAACCTTCAAGAAAGTA 4500
 QY 4501 GTGAATTAACCTTAAGCCAGATCCAGAGGCTTCTGCTGACAGTTTGAAGGTCTG 4560
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 QY 4561 CAGATAGTCTTACAGATAAAATTAAGAACCAAGAGTGAAGAGTATCCCTTCTTAAT 4620
 Db 4561 CAGATAGTCTTACAGATAAAATTAAGAACCAAGAGTGAAGAGTATCCCTTCTTAAT 4620
 QY 4621 GCCCATCATTAATAGTATAGGTGTATCATCACAGTGTCTGAGGAGTCTTCAAAATGAA 4680
 Db 4621 GCCCATCATTAATAGTATAGGTGTATCATCACAGTGTCTGAGGAGTCTTCAAAATGAA 4680
 QY 4681 ACTACCCATCTGACAGAGGACTCATTAAGTTGTGATGTGAGGACCAAGCTGGAAG 4740
 Db 4681 ACTACCCATCTGACAGAGGACTCATTAAGTTGTGATGTGAGGACCAAGCTGGAAG 4740
 QY 4741 AGCTGGGACACAGATTTGACGGAACAATCTTACTTGGCCAGCAAGATCTTAGAGGAA 4800
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 QY 4801 CCCCTTAACCTGGAATTTGGAATCAGCTCTTCTGATGACCTGGAATCTGATCTTCTG 4860
 Db 4801 CCCCTTAACCTGGAATTTGGAATCAGCTCTTCTGATGACCTGGAATCTGATCTTCTG 4860

QY 4861 AAGACAGACCCACAGAGTCACTGCTGTGTGGCAACATACCATCTTCAACCTCTGCAATGA 4920
 Db 4861 AAGACAGACCCACAGAGTCACTGCTGTGTGGCAACATACCATCTTCAACCTCTGCAATGA 4920
 QY 4921 AAGTTCCCAATTTGAAGTTGAGATTTGCTCCAGAGTCCAGTGTCTGTATCTACTG 4980
 Db 4921 AAGTTCCCAATTTGAAGTTGAGATTTGCTCCAGAGTCCAGTGTCTGTATCTACTG 4980
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 Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAATGTGAGCAGGAGAGACAGAAATTTGACAG 5040
 QY 5041 CTTCAACAGAAAGGCTCAACAAAGATATGCTATGCTGTGTGCTGCTGACCCAGAG 5100
 Db 5041 CTTCAACAGAAAGGCTCAACAAAGATATGCTATGCTGTGTGCTGCTGACCCAGAG 5100
 QY 5101 AATTATCTGCTGTGACAAATTTGCTGACAAACACACATCATCTTAACTTAATTA 5160
 Db 5101 AATTATCTGCTGTGACAAATTTGCTGACAAACACACATCATCTTAACTTAATTA 5160
 QY 5161 CTGAAGACATCACTCATGTTGTATGAAACAGATGCTGAGTTGTGTGAAACGACAC 5220
 Db 5161 CTGAAGACATCACTCATGTTGTATGAAACAGATGCTGAGTTGTGTGAAACGACAC 5220
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 Db 5221 TGAATATTTTCTAGAAATTCGGGAGGAAATGAGTATGCTATTTCTGAGTACC 5280
 QY 5281 AGCTATTTAAAGAAAGAAATTTGCTGAATGACATGATTTTGAAGTCAAGAGAGATGCG 5340
 Db 5281 AGCTATTTAAAGAAAGAAATTTGCTGAATGACATGATTTTGAAGTCAAGAGAGATGCG 5340
 QY 5341 TCAATGGAAGAAACCAACAGGCTCCAAAGCAGACAGAAATCCAGACAGAAAGTCT 5400
 Db 5341 TCAATGGAAGAAACCAACAGGCTCCAAAGCAGACAGAAATCCAGACAGAAAGTCT 5400
 QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCAACCAATGCCACAGATCACTGG 5460
 Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCAACCAATGCCACAGATCACTGG 5460
 QY 5461 AATGATGGTACAGCTGTGTGTGCTTCTGTGTGAGAGACCTTTCATTCACCTTG 5520
 Db 5461 AATGATGGTACAGCTGTGTGTGCTTCTGTGTGAGAGACCTTTCATTCACCTTG 5520
 QY 5521 GCACAGGTGTCACCAATTTGTTGTGTCAGCCAGATGCTGACAGAGCAATGGCT 5580
 Db 5521 GCACAGGTGTCACCAATTTGTTGTGTCAGCCAGATGCTGACAGAGCAATGGCT 5580
 QY 5581 TCCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTGTTGACA 5640
 Db 5581 TCCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTGTTGACA 5640
 QY 5641 GTGTAGCACTTACCAAGTGCAGAGGCTGACACCTTACTGATACCCCAATGCCACA 5700
 Db 5641 GTGTAGCACTTACCAAGTGCAGAGGCTGACACCTTACTGATACCCCAATGCCACA 5700
 QY 5701 GCCACTACTGA 5711
 Db 5701 GCCACTACTGA 5711

RESULT 4
 US-09-982-828-3
 ; Sequence 3, Application US/09982828
 ; Publication No. US20030022184A1
 ; GENERAL INFORMATION:
 APPLICANT: Murphy, Patricia D.
 Allen, Antonette C.
 Alvarez, Christopher P.
 Cirtz, Brenda S.
 Olson, Sheri J.
 Thurber, Denise
 Zeng, Bin

TITLE OF INVENTION: Coding Sequences of the Human
BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,828
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/074,453
FILING DATE: 1998-05-06
APPLICATION NUMBER: US 08/798,691
FILING DATE: 1997-02-12
APPLICATION NUMBER: US 08/598,591
FILING DATE: 1996-02-12
ATTORNEY/AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
REFERENCE/DOCKET NUMBER: 44921-5053-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om12)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-982-828-3
Query Match 99.9%; Score 5703; DB 9; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 301 GTCTTTATGTGAAGATGATATATACCAAAAGAGCCTTACAGAAAGTACGAGATTAGTC 360
QY 361 AACTGTGTGAAGAGCTATTTGAAAATATTTGGCTTTTCAAGCTTGACACAGGTTTGAGT 420
DB 361 AACTGTGTGAAGAGCTATTTGAAAATATTTGGCTTTTCAAGCTTGACACAGGTTTGAGT 420
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DB 421 ATGCAGAGCTATATATTTTGCAGAAAAGAAAATTAAGTCTCCTGTAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTTTACAGAGT 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTTTACAGAGT 540
QY 541 AACCCGAAAATCCTTCTTGACAGAAAACCAAGTCTCAGTCTCAACTCTTAACCTTGAA 600
DB 541 AACCCGAAAATCCTTCTTGACAGAAAACCAAGTCTCAGTCTCAACTCTTAACCTTGAA 600
QY 601 CTGTGAGAACTCTGAGAGCAAAAGCAGCGGATCAACCTGCAAAAAGAGCTGTACATTTG 660
DB 601 CTGTGAGAACTCTGAGAGCAAAAGCAGCGGATCAACCTGCAAAAAGAGCTGTACATTTG 660
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DB 661 AATTGGGATCTGATTTCTTCTGAAAGATACCGTTAATAGCAACTTATTCAGAGTGGAG 720
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DB 781 CAAAAAGGCTGCTGTGAATTTTCTGAGACGGATTAACAAATCACTGAACATCATCAAC 840
QY 841 CCAGTAATATGATTTTGAACACCACTGAGAACGCTGACCTGAGAGCATCCAGAAAGT 900
DB 841 CCAGTAATATGATTTTGAACACCACTGAGAACGCTGACCTGAGAGCATCCAGAAAGT 900
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DB 901 ATCAGGGATGTTCTGTTTCAAACTTGATGTGAGAGCCATGTGGCAAAATATCTCATGCCA 960
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DB 1021 AAGCTGAATTTCTGTATATAAAGCAAAACAGCTGTGTACAGAGAGCCAAATACAGAT 1080
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QY 1141 ATCTGAATGCTATCCCTGCTGTGAGAGAAAGATGAATGAAGCAAACTGCCATGCT 1200
DB 1141 ATCTGAATGCTATCCCTGCTGTGAGAGAAAGATGAATGAAGCAAACTGCCATGCT 1200
QY 1201 CAGAGATCTGAGATACGTAAAGATGTCTTGTGATACACTTAATATACAGATTCAGAG 1260
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Qy 1561 TAAATTAAGAGAGATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAATA 1620
Db 1561 TAAATTAAGAGAGATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAATA 1620
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Db 1621 AATTAAGCCGTAAAGAGAGCCTACATCAGGCTTCATCCTGAGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATATAATCAGGAACTAAACCAAGCGAGC 1740
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Qy 1741 AGAATGGTCAAGTGAATGATATTAATTAATAGTGTCTATGAGAAATAACAAAAGGTGATT 1800
Db 1741 AGAATGGTCAAGTGAATGATATTAATTAATAGTGTCTATGAGAAATAACAAAAGGTGATT 1800
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Db 1801 CTATTCAGATGAGAAAATCTCTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTTA 1860
Qy 1861 AAACGAAAGCTGAACCTTAATAGCAGAGATATAGCAATATGGAATCGAATTAATATCC 1920
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Qy 1921 ACAATTCAAAAGACCTTAAAGAAATAGGCTGAGAGAGAAAGCTTCTTACAGGCAATATTC 1980
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Qy 1981 ATGGGCTTGAATAGTACTAGTACGTAAGAAATCTAAGCCCACTAATTTGTAATTTGCCAA 2040
Db 1981 ATGGGCTTGAATAGTACTAGTACGTAAGAAATCTAAGCCCACTAATTTGTAATTTGCCAA 2040
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QY 4561 CAGATAGTCTTACAGTAAATTAAGAACAGAGTGAAGAGTCACTCCCTTTCTTAAT 4620
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QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 5
US-10-022-819-1
Sequence 1, Application US/10022819
Publication No. US20030027166A1
GENERAL INFORMATION:
APPLICANT: ALLEN, Antoinette C. P.
OLSEN, Sheri J.
LAWRENCE, Tammy
ANGELLY, Tracy S.
RABIN, Mark B.
TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
BRCA1 GENE
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue
CITY: Washington DC
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/022,819
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,452
FILING DATE: 1998-05-06
ATTORNEY/AGENT INFORMATION:
NAME: <Unknown>
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 044921-5049-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3001
TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
HAPLOTYPE: OM14
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-022-819-1
Query Match 99.9%; Score 5703; DB 9; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCTGCGTGAAGCTTCTGGAGCCCGCACAGGCTGTGGGGTTTCTCAGATTAACATGGGCC 60
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DB 61 CCTGCGCTCAGAGAGGCTTCAACCTCTGCTTGGGTAAGTTCATTTGGAAGAGAGAGAA 120
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DB 361 AACTGTGAAGAGCTATTTGAATAATCTTTGCTTTTCAGCTTGACAGAGTTGGAGT 420
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DB 841 CCAATTAATTAATGATTTGAACCACTGAGAGAGGCTGAGCTGAGAGGCAATCCAGAAAGT 900
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QY 1381 AATATTCTGGTTCTTACAGAGAAATGACTTACCTGGCAGAGTATCCCATGAGGCTTTAA 1440
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QY 1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGGAAAGTCTTACACGACATATTC 1980
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Db 5701 GCCACTACTGA 5711
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RESULT 6
US-09-734-672-1
Sequence 1, Application US/09734672
Publication No. US20020183268A1
GENERAL INFORMATION:
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Allen, Antoinette C.
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TITLE OF INVENTION: Coding Sequences of the Human
BRCAl Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Ave., N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 03-Dec-2000
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: No. US20020183268A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAl
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-734-672-1
Query Match 99.8%; Score 5701.4; DB 9; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 1921 ACAATTTCAAAAGCACTTAATAAGATAGGCTGAGAGAGAGTCTTCTACAGGCAATATC 1980
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Db 5701 GCCACTACTGA 5711

RESULT 7

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TITLE OF INVENTION: Coding Sequences of the Human
BRCA1 Gene

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESSES:

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,828
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>

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FILING DATE: 1996-02-12

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

STRAIN: BRCA1 (om11)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-982-828-1
Query Match 99.8%; Score 5701.4; DB 9; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 2761 AATGTCAACATTTCTGCCCCACTGCGGCTCTTAAAGAAACAAAGTCCAAAAGCACTT 2820
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Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATCTAATATCAAGCTGTAC 2880
Qy 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTGTGTGTAGAAAGATTAAGCCAGTTGAT 2940
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTGTGTGTAGAAAGATTAAGCCAGTTGAT 2940
Qy 2941 ATGCCAAATGTATCAAGAGAGGCTAGGTTTGTATATCATCTCAGTCCAGAGGCA 3000
Db 2941 ATGCCAAATGTATCAAGAGAGGCTAGGTTTGTATATCATCTCAGTCCAGAGGCA 3000
Qy 3001 ACGAAACTGAGCTTACTTCCAAATTAACATGAGCTTTTACAAACCCATATCGTATAC 3060
Db 3001 ACGAAACTGAGCTTACTTCCAAATTAACATGAGCTTTTACAAACCCATATCGTATAC 3060
Qy 3061 CACCACTTTTCCCATCAAGTATTTGTTAAACTTAATATGTAAGAAAAATCTGCTAGAG 3120
Db 3061 CACCACTTTTCCCATCAAGTATTTGTTAAACTTAATATGTAAGAAAAATCTGCTAGAG 3120

QY 3121 AAACTTTGAGGAACATTCATGTGCACTGAAAGAAATGGGAAATGAGAACTATCCAA 3180
DB 3121 AAACTTTGAGGAACATTCATGTGCACTGAAAGAAATGGGAAATGAGAACTATCCAA 3180
QY 3181 GTACAGTACGACAAATTAGCCCTGAATACATTAGAGAAATGTTTTTAAAGAACCACT 3240
DB 3181 GTACAGTACGACAAATTAGCCCTGAATACATTAGAGAAATGTTTTTAAAGAACCACT 3240
QY 3241 CAAGCAATTAATTAAGAGGTTCCAGTAAATGAATGGGCTCAGTATTAATGAAA 3300
DB 3241 CAAGCAATTAATTAAGAGGTTCCAGTAAATGAATGGGCTCAGTATTAATGAAA 3300
QY 3301 TAGGTTCCAGTATGAAAAATTCAGAGAACTAGTAGAAAACAGAGGCCAAATTA 3360
DB 3301 TAGGTTCCAGTATGAAAAATTCAGAGAACTAGTAGAAAACAGAGGCCAAATTA 3360
QY 3361 ATGCTATGCTTAGATTAGGGGTTTGGCACTGAGGCTTAATAACAAAGCTTTCTGGA 3420
DB 3361 ATGCTATGCTTAGATTAGGGGTTTGGCACTGAGGCTTAATAACAAAGCTTTCTGGA 3420
QY 3421 GTAATTGTAAGCATCTGAAATTAATAAGCAAGAAATATGAGAGAGTTCAGACTGTA 3480
DB 3421 GTAATTGTAAGCATCTGAAATTAATAAGCAAGAAATATGAGAGAGTTCAGACTGTA 3480
QY 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAATTAAGCAAGCTTATGGAGTAGTC 3540
DB 3481 ATACAGATTTCTCTCCATATCTGATTTAGATTAATTAAGCAAGCTTATGGAGTAGTC 3540
QY 3541 ATGCTATGCTTAGATTAGGGGTTTGGCACTGAGGCTTAATAACAAAGCTTTCTGGA 3600
DB 3541 ATGCTATGCTTAGATTAGGGGTTTGGCACTGAGGCTTAATAACAAAGCTTTCTGGA 3600
QY 3601 AAGACTAGTTTCTGTAATAATGACATTAAGAAAGTCTGCTGTTTTTACAAAGG 3660
DB 3601 AAGACTAGTTTCTGTAATAATGACATTAAGAAAGTCTGCTGTTTTTACAAAGG 3660
QY 3661 TCCAGAAAGAGAGGCTTAGCAGAGAGTCTAGGCTTTCAACCATAACATTTGGCTCAG 3720
DB 3661 TCCAGAAAGAGAGGCTTAGCAGAGAGTCTAGGCTTTCAACCATAACATTTGGCTCAG 3720
QY 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGTCTCAGAGAGAACTTATTAAGTAGATG 3780
DB 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGTCTCAGAGAGAACTTATTAAGTAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCAACACTGTTATTTGGTAAAGTAAACAATATACCTTCAGT 3840
DB 3781 AAGAGCTTCCCTGCTTCAACACTGTTATTTGGTAAAGTAAACAATATACCTTCAGT 3840
QY 3841 CTACTAGGCATAGCAACCGTTGCTACGAGTGTCTGTCTAAGAAACACAGAGAAATTA 3900
DB 3841 CTACTAGGCATAGCAACCGTTGCTACGAGTGTCTGTCTAAGAAACACAGAGAAATTA 3900
QY 3901 TATCATTTGAAGAAATGCTTAAATGACTGAGTAACTCAGAGTAAATTTGGCAAGGCACTTC 3960
DB 3901 TATCATTTGAAGAAATGCTTAAATGACTGAGTAACTCAGAGTAAATTTGGCAAGGCACTTC 3960
QY 3961 AGGAACATCACTTGAAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCCAGTGA 4020
DB 3961 AGGAACATCACTTGAAGAGAAACAAATGTTCTGCTAGCTGTTTCTTCCAGTGA 4020
QY 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACACCCAGAGTCTTTCTTATTTGTTCTT 4080
DB 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACACCCAGAGTCTTTCTTATTTGTTCTT 4080
QY 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGAGGAGTTGCTGAGTGAACAAGAAATGG 4140
DB 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGAGGAGTTGCTGAGTGAACAAGAAATGG 4140
QY 4141 TTTGAGATGATGAAGAAAGAGGAGCGGCTTGAAGAAATATCAAGAAAGCAAGGA 4200
DB 4141 TTTGAGATGATGAAGAAAGAGGAGCGGCTTGAAGAAATATCAAGAAAGCAAGGA 4200
QY 4201 TGAATTCAAACTTAGTGAGAGCAGCATCTGGGTGTGAGAGTGAACAAAGCTCTGTAAG 4260

DB 4201 TGAATTCAAACTTAGTGAGAGCAGCATCTGGGTGTGAGAGTGAACAAAGCTCTGTAAG 4260
QY 4261 ACTGCTCAGGCTATACCTCTCAGAGTGAATTTTAAACCACTCAGAGAGGATCACTG 4320
DB 4261 ACTGCTCAGGCTATACCTCTCAGAGTGAATTTTAAACCACTCAGAGAGGATCACTG 4320
QY 4321 AACATAACCTGATTAAGCTCCAGAGAGAAATGAGTGAATTAAGTGTGTTAAGACAGC 4380
DB 4321 AACATAACCTGATTAAGCTCCAGAGAGAAATGAGTGAATTAAGTGTGTTAAGACAGC 4380
QY 4381 ATGGAGCCAGCTTTCTAAGCTTACCTTCAATCAATAGTACTCTTCTGCTTGAAG 4440
DB 4381 ATGGAGCCAGCTTTCTAAGCTTACCTTCAATCAATAGTACTCTTCTGCTTGAAG 4440
QY 4441 ACCTGCGAAATCCGAAACAAAGCAGATGAGAAAGAGATTTAAGTCTTCCAGAAAGTA 4500
DB 4441 ACCTGCGAAATCCGAAACAAAGCAGATGAGAAAGAGATTTAAGTCTTCCAGAAAGTA 4500
QY 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTGTGCTG 4560
DB 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTGTGCTG 4560
QY 4561 CAGATAGTTCTTACGATTAATAAAGAACAGAGTGAAGAGTCAATCCCTTTCTAAT 4620
DB 4561 CAGATAGTTCTTACGATTAATAAAGAACAGAGTGAAGAGTCAATCCCTTTCTAAT 4620
QY 4621 GCGCCATCTTGAATGATGAGTGTGATCATGCACTGCTGCTGAGAGTCTTCAAGAAATGA 4680
DB 4621 GCGCCATCTTGAATGATGAGTGTGATCATGCACTGCTGCTGAGAGTCTTCAAGAAATGA 4680
QY 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGATGAGTGAAGAGCAACAGCTGGAAG 4740
DB 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGATGAGTGAAGAGCAACAGCTGGAAG 4740
QY 4741 AGTCTGGGCCACAGATTTGACGAAACATTTACTTCCAGAGCAAGATCTAGAGGAA 4800
DB 4741 AGTCTGGGCCACAGATTTGACGAAACATTTACTTCCAGAGCAAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTGCTGAGACCCGATCTGATCTCTG 4860
DB 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTGCTGAGACCCGATCTGATCTCTG 4860
QY 4861 AAGACAGAGCCCAAGAGTCACTGCTGTTGGCAATACATCTTCAACCTCTGCAATGA 4920
DB 4861 AAGACAGAGCCCAAGAGTCACTGCTGTTGGCAATACATCTTCAACCTCTGCAATGA 4920
QY 4921 AAGTTCGCCAATTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATCTACTG 4980
DB 4921 AAGTTCGCCAATTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATCTACTG 4980
QY 4981 ATACTGCTGGGATTAATGCAATGGAAGAAATGAGAGAGGAGAGACCAAGATTTGACAG 5040
DB 4981 ATACTGCTGGGATTAATGCAATGGAAGAAATGAGAGAGGAGAGACCAAGATTTGACAG 5040
QY 5041 CTTCAACGAAAGGGTCAACAAAGAAATGTCATGCTGCTGCTGAGCTGAGCCCAAGAG 5100
DB 5041 CTTCAACGAAAGGGTCAACAAAGAAATGTCATGCTGCTGAGCTGAGCCCAAGAG 5100
QY 5101 AATTATGCTGCTGATCAAGATTTGCCAGAAACACACATCACTTAATTAATTAATTA 5160
DB 5101 AATTATGCTGCTGATCAAGATTTGCCAGAAACACACATCACTTAATTAATTAATTA 5160
QY 5161 CTGAAGAGATCACTCATGCTTGTATGAAACAGATGCTGAGTGTGTGTAAGGAGCAC 5220
DB 5161 CTGAAGAGATCACTCATGCTTGTATGAAACAGATGCTGAGTGTGTGTAAGGAGCAC 5220
QY 5221 TGAATATTTTCTGGAATTTGCGGAGAGAAATGGTATGATTTTCTGAGTGAAGCC 5280
DB 5221 TGAATATTTTCTGGAATTTGCGGAGAGAAATGGTATGATTTTCTGAGTGAAGCC 5280
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAAGAGAGATGAG 5340


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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4552
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78833.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; US-09-864-761-4552

Query Match          3.1%; Score 175.4; DB 10; Length 424;
Best Local Similarity 94.3%; Pred. No. 2e-34; Mismatches 11; Indels 0; Gaps 0;
Matches 182; Conservative 0;

QY 4303 AGCAGAGGATACATGACATACCTGATTAAGCTCCAGAGGAAATGGCTGAAGTAG 4362
    |||||
DB 232 AGCAGAGGATACATGACATACCTGATTAAGCTCCAGAGGAAATGGCTGAAGTAG 291
    |||||
QY 4363 AAGCTGTATTAGAACAGATGGAGGACCTTTTACAGCTTACCTTCATCATTAAGTG 4422
    |||||
DB 292 AAGCTGTATTAGAACAGATGGAGGACCTTTTACAGCTTACCTTCATCATTAAGTG 351
    |||||
QY 4423 ACTCTTGTGCTTGTAGGACCTGCGAAATCCAGAACAAAGCATCAGAAAAAGCAGTAT 4482
    |||||
DB 352 ACTCTTGTGCTTGTAGGACCTGCGAAATCCAGAACAAAGCATCAGAAAAAGTGTGT 411
    |||||
QY 4483 TAACCTTCACAGAA 4495
    |||||
DB 412 ATTGTGTGCCAA 424
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RESULT 10
US-09-864-761-21299
; Sequence 21299, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmice-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21299
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78833.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EST HUMAN HIT: AUI25312.1, EVALUE 2.00e-77
; OTHER INFORMATION: SWISSPROT HIT: P38398, EVALUE 4.00e-12
; OTHER INFORMATION: NT HIT: g11424969, EVALUE 1.00e-77
; US-09-864-761-21299

Query Match          2.6%; Score 147; DB 10; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.8e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 147; Conservative 0;

QY 4330 TGATTAAGCTCCAGAGGAAATGGCTGACATGAGAGCTGTGAGACAGATGGAGGCC 4389
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DB 1 TGATTAAGCTCCAGAGGAAATGGCTGACATGAGAGCTGTGAGACAGATGGAGGCC 60
    |||||
QY 4390 AGCTTCTTACAGGATACCTTCCATCATTAAGTGAAGTCTTCTGCTTGAAGACCTGGAA 4449
    |||||
DB 61 AGCTTCTTACAGGATACCTTCCATCATTAAGTGAAGTCTTCTGCTTGAAGACCTGGAA 120
    |||||
QY 4450 ATCCAGAACAAAGCATCAGAAAAAG 4476
    |||||
DB 121 ATCCAGAACAAAGCATCAGAAAAAG 147
    |||||

RESULT 11
US-09-818-875-653
; Sequence 653, Application US/0981875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gampert, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
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Qy	62	CTGGGCTCAGAGAGGCTTACCCCTCTGGCTCTGGGTAAGAGTTATCTGGAAACGAAAGAAAT	121
Dd	121	CTGGGCTCAGAGAGGCTTACCCCTCTGGCTCTGGGTAAGAGTTATCTGGAAACGAAAGAAAT	62
Qy	122	GGATTATCTGCTCTTGGCGGTGAGAAAGTACAAAATGTCAATTAATGCTATGCGAAAAAT	181
Dd	61	GGATTATCTGCTCTTGGCGGTGAGAAAGTACAAAATGTCAATTAATGCTATGCGAAAAAT	2
Qy	-	182 C 182	

[illegible]

Sequence 658, Application US/09818875
Publication No. US20030051270A1
GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Gamcer, Howard B.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/09/818, 875
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedman macro Napro4
SEQ ID NO 658

LENGTH: 121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-818-875-658

Query Match 2.1%; Score 121; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.1e-21;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CTGGGTAAGTTCATTGGACAGAAATGATTTATCTGCTTCCTCGGTTGAAGAAG 150
DB 121 CTGGGTAAGTTCATTGGACAGAAATGATTTATCTGCTTCCTCGGTTGAAGAAG 62
QY 151 TACAAATGTCATTATGCTATGTCAGAAATCTTAGAGTGTCCCATCTGCTGAGTTGA 210
DB 61 TACAAATGTCATTATGCTATGTCAGAAATCTTAGAGTGTCCCATCTGCTGAGTTGA 2

QY 211 T 211
DB 1 T 1

RESULT 15
US-09-818-875-661
Sequence 661, Application US/09818875
Publication No. US20030051270A1
GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/09/818,875
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedmann macro Napro4
SEQ ID NO 661
LENGTH: 121
TYPE: DNA
ORGANISM: Homo sapiens
US-09-818-875-661

Query Match 2.1%; Score 121; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.1e-21;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ATGATTTATCTGCTTCGCTTGAAGATGACAAATGCTATTAATGCTATGACAGAA 179
DB 1 ATGATTTATCTGCTTCGCTTGAAGATGACAAATGCTATTAATGCTATGACAGAA 60
QY 180 ATCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGAACTGTCTCCACAAAGTGTGAC 239
DB 61 ATCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGAACTGTCTCCACAAAGTGTGAC 120
QY 240 C 240
DB 121 C 121

Search completed: June 13, 2003, 12:45:45
Job time : 727.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:09:35 ; Search time 14037.5 Seconds

(without alignments)
11840.151 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711
Sequence: 1 AGCTCGCTAGACTCTCTG3.....TCCCCACAGCAGCTACTGA 5711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl: 1: gb_ba: 2: gb_hcg: 3: gb_in: 4: gb_cm: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pac: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_hcg_hum: 31: em_hcg_inv: 32: em_hcg_ocher: 33: em_hcg_mus: 34: em_hcg_pln: 35: em_hcg_rtd: 36: em_hcg_mam: 37: em_hcg_vrt: 38: em_sy: 39: em_hcgo_hum: 40: em_hcgo_mus: 41: em_hcgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5711	100.0	5711	6	AR007334	AR007334 Sequence
2	5711	100.0	5711	6	AR112810	AR112810 Sequence
3	5709.4	100.0	5711	6	AR033056	AR033056 Sequence
4	5709.4	100.0	5711	9	HSU14680	U14680 Homo sapien
5	5709.4	100.0	5712	6	AR070223	AR070223 Sequence
6	5709.4	100.0	5712	6	AR118507	AR118507 Sequence
7	5709.4	100.0	5712	6	AR125601	AR125601 Sequence
8	5709.4	100.0	5712	6	AR184044	AR184044 Sequence
9	5709.4	100.0	5914	6	AR004673	AR004673 Sequence
10	5709.4	100.0	5914	6	AR008159	AR008159 Sequence
11	5709.4	100.0	5914	6	AR136942	AR136942 Sequence
12	5709.4	100.0	5914	6	176943	176943 Sequence 1
13	5709.4	100.0	5914	6	180938	180938 Sequence 1
14	5709.4	100.0	5914	6	181034	181034 Sequence 1
15	5707.8	99.9	5711	6	AR048660	AR048660 Sequence
16	5707.8	99.9	5711	6	AR048666	AR048666 Sequence
17	5707.8	99.9	5711	6	140795	140795 Sequence 4
18	5707.8	99.9	5711	6	140801	140801 Sequence 4
19	5703	99.9	5711	6	AR007335	AR007335 Sequence
20	5703	99.9	5711	6	AR112809	AR112809 Sequence
21	5701.4	99.8	5711	6	AR007333	AR007333 Sequence
22	5701.4	99.8	5711	6	AR112808	AR112808 Sequence
23	5701.4	99.8	5711	6	159546	159546 Sequence 1
24	5698.4	99.8	5712	6	AR048668	AR048668 Sequence
25	5698.4	99.8	5712	6	140803	140803 Sequence 12
26	5697.4	99.8	5710	6	AR048662	AR048662 Sequence
27	5697.4	99.8	5710	6	140797	140797 Sequence 6
28	5695.4	99.7	5709	6	AR048658	AR048658 Sequence
29	5695.4	99.7	5709	6	AR048653	AR048653 Sequence
30	5695.4	99.7	5709	6	AR048664	AR048664 Sequence
31	5695.4	99.7	5709	6	AR048665	AR048665 Sequence
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33	5695.4	99.7	5709	6	140798	140798 Sequence 7
34	5695.4	99.7	5709	6	140799	140799 Sequence 8
35	5695.4	99.7	5709	6	140800	140800 Sequence 9
36	5691.4	99.7	5707	6	AR048667	AR048667 Sequence
37	5691.4	99.7	5707	6	140802	140802 Sequence 11
38	5659.4	99.1	5709	6	AX281859	AX281859 Sequence
39	5655.4	99.0	5689	6	AR048659	AR048659 Sequence
40	5655.4	99.0	5689	6	140794	140794 Sequence 3
41	5629.2	98.6	5770	6	AR048661	AR048661 Sequence
42	5629.2	98.6	5770	6	140796	140796 Sequence 5
43	5590.4	97.9	5656	6	AR048657	AR048657 Sequence
44	5590.4	97.9	5656	6	140792	140792 Sequence 1
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ALIGNMENTS

RESULT 1
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LOCUS AR007334 Sequence 3 from patent US 5750400.
DEFINITION AR007334
ACCESSION AR007334.1 GI:3966818
VERSION AR007334.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,
Schelter,D.B. and Zeng,B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 5750400-A 3 12-MAY-1998;

FEATURES
source 1. 5711
Location/Qualifiers
/organism="unknown"
BASE COUNT 1956 a 1098 c 1274 g 1383 t
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTCTTCGAGACCCGACACAGGCTGTGGGGTTTCTCAGATACCTGGCC 60
DB 1 AGCTGCTGAGACTCTTCGAGACCCGACACAGGCTGTGGGGTTTCTCAGATACCTGGCC 60
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DB 61 CCTGGCTGAGAGGCTTCAACCCCTCTGCTGGTAAAGTTCATGGAGAGAGAGAA 120
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DB 121 TGAATTTATCTGCTCTTCGCGTTGAGAGATACAAATGTCAATTAATGCTATGAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTGATGAGAACTGTCCACAAAGTGTACC 240
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTGATGAGAACTGTCCACAAAGTGTACC 240
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DB 241 ACATATTTTGCAGAAATTTTGCATGTGAGAACTCTCACAGAGAGAGAGGCTTCACAGT 300
QY 301 GTCTTTATGTAGAGATATATACCAAGAGGCTTACAGAGAGATGAGATTTAGTC 360
DB 301 GTCTTTATGTAGAGATATATACCAAGAGGCTTACAGAGAGATGAGATTTAGTC 360
QY 361 AACTGTGAGAGAGATATGAGAAATCATTTTGTCTTTCAGCTTGACACAGTTGGAGT 420
DB 361 AACTGTGAGAGAGATATGAGAAATCATTTTGTCTTTCAGCTTGACACAGTTGGAGT 420
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DB 421 ATGCAACAGCTATATATTTTGCAGAAAGAGAAATTAATCTCTCTGACATCTTAAAGATG 480
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DB 541 AACCCGAAATCCCTTCTCTGAGAGAAACCAAGTCTAGAGTCCAACTCTCTAACTTTGGA 600
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QY 1861 AAAG 1920
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RESULT 2
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 VERSION AR112810.1 GI:14092710
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5711)
 AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,
 Thurber, D., and Zeng, B.
 TITLE Coding sequences of the human BRCA1 gene
 JOURNAL Patent, US 6130322-A 5 10-OCT-2000;
 FEATURES
 source Location/Qualifiers
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 BASE COUNT 1956 a 1098 c 1274 g 1383 t
 ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGCTGAGACTCTCTGAGACCCGACAGGCTGTGGGTTTCTCAGATTAATGAGGCC 60
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QY 1681 CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCGAGAACTTAAACGAGAGC 1740
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QY 1861 AAACGAAAGCTGAACCTTAATAGCAGCAGTATAGCAATATGGAATCTGAAATTAATTC 1920
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Db 1921 ACAATTTCAAAAGCAGCTTAAAAAGAAATAGGCTGAGAGGAAAGTCTTCAACAGCATATTC 1980
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Db 2101 GGCACAGCAGAAACCTAACAATCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
QY 2161 GTTAACAGCCAAATGAACAGCACTAATAAAGCATGACAGCGATACTTTCCAGAGCTGA 2220
Db 2161 GTTAACAGCCAAATGAACAGCACTAATAAAGCATGACAGCGATACTTTCCAGAGCTGA 2220
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Db 2341 CTAAATTAATGCTGAAGACCCCAAAAGATCTCATGTTAAGTGAAGAAAGGTTTGCACATG 2400
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Db	2461	AAAAGTATCTCGTTACTGTAAGAGTTAGCACTCTAGGGAAGGCAAAAACGAAACCAATAAT	252
QY	2521	GGTGTAGTCAGTGTGCGAGCATTTTGAAAACCCCAAGGGGCTAAATTCATGGTGTTCGAAAG	258
Db	2521	GGTGTAGTCAGTGTGCGAGCATTTTGAAAACCCCAAGGGGCTAAATTCATGGTGTTCGAAAG	258
QY	2581	ATPATGAAATGACACAGAAAGGCTTTAAGTATTCATTGGGACATGAAGTTAACCAAGTC	264
Db	2581	ATPATGAAATGACACAGAAAGGCTTTAAGTATTCATTGGGACATGAAGTTAACCAAGTC	264
QY	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAATATTTGCAAAATACAT	270
Db	2641	GGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAATATTTGCAAAATACAT	270
QY	2701	TCGAAGTTTCAAGCGCCGACATCTTGTCTCTGTTTCAATCCAGAGAAATCAGAAAGG	276
Db	2701	TCGAAGTTTCAAGCGCCGACATCTTGTCTCTGTTTCAATCCAGAGAAATCAGAAAGG	276
QY	2761	AATGTGCACATTTCTGTGCCACTCTGGGTCCTTAAAGAAACAAGTCGCACTT	282
Db	2761	AATGTGCACATTTCTGTGCCACTCTGGGTCCTTAAAGAAACAAGTCGCACTT	282
QY	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC	288
Db	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC	288
QY	2881	AGACAGTTATATCACTGACAGGCTTCTGTGGTGTGTCAGAAAGATTAAGCAGTTGATA	294
Db	2881	AGACAGTTATATCACTGACAGGCTTCTGTGGTGTGTCAGAAAGATTAAGCAGTTGATA	294
QY	2941	ATGCCAAATGTAGTATCAAGAGAGGCTTAAGTTTTGTATCATCTCAGTTCAAGGCA	300
Db	2941	ATGCCAAATGTAGTATCAAGAGAGGCTTAAGTTTTGTATCATCTCAGTTCAAGGCA	300
QY	3001	ACGAAACTGGAATCTTACTCTCCAAATAAACATGACCTTTTCAAAACCCCATATGTATAC	306
Db	3001	ACGAAACTGGAATCTTACTCTCCAAATAAACATGACCTTTTCAAAACCCCATATGTATAC	306
QY	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAAACTAATGTATGAAGAAATCTGCTAGAG	312
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAAACTAATGTATGAAGAAATCTGCTAGAG	312
QY	3121	AAAACCTTGAGAAACATTCATATGTCACCTGAAAGAAATGGAATGAGAACTTCCAA	318
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QY	3241	CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGTATTTATGAAA	330
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Db	3301	TAGGTTCCAGTGAAGAAACATTCAGACAGAACTAAGTAGAAACAGAGGCAAAATTTGA	336
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCACTGAGGTCATATAACAAAGTTTCTCTGGA	342
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QY	3421	GTATATGTAGCAATCCGAATATAAAGACAGAAATGAAGAGTGTTCAGACTGTTA	348
Db	3421	GTATATGTAGCAATCCGAATATAAAGACAGAAATGAAGAGTGTTCAGACTGTTA	348
QY	3481	ATACAGATTTCTCCATATCTGATTTCAATTAATTAGAACACGCTATGGAAGTAGTC	354
Db	3481	ATACAGATTTCTCCATATCTGATTTCAATTAATTAGAACACGCTATGGAAGTAGTC	354
QY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACTCTGTTAGATGATGTGAAATTAAGG	360

Db	3541	ATGCACTCAGGGTTGTGTTCTGAGACACCTGATGACCTGTTTAGATGATGGTGAATTAAAGC	3600
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Db	3601	AAGACTACTAGTTTGTCTGAAAAATACATTTAAGAAAGTTTGTGCTGTTTTAGCAAAAGCG	3660
QY	3661	TCGAAAGAGAGAGCTTNGCAGAGTCTTAGCCCTTTTCAACCATACATTTGGCTCAGG	3720
Db	3661	TCGAAAGAGAGAGCTTNGCAGAGTCTTAGCCCTTTTCAACCATACATTTGGCTCAGG	3720
QY	3721	GTTACCGAAGAGGGGGCCAGAAATTTAGAGTCTCAGAAAGAGACTTATCTTAGAGAGTGG	3780
Db	3721	GTTACCGAAGAGGGGGCCAGAAATTTAGAGTCTCAGAAAGAGACTTATCTTAGAGAGTGG	3780
QY	3781	AAGAGCTTCCCTGCTTCCACACCTGTGTTATTTGGTAAAGTAAACAATAATACCTTCTCAGT	3840
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Db	3961	AGGAACATCACCTTAGTAGAGGAAACAAATGTTCTGTAGCTGTTTTCTTTCACAGTGCA	4020
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QY	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA	4200
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Db	4201	TGGAATTCAACTTAGTGAAGACAGACATCTGGGGTGTGAAGTGAACAAAGCTCTCTGAAG	4260
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Db	4261	ACTGTGAGGGGCTATCCTCTCAGAGTACATTTTAACAACCTCAGCAGAGGGGATACCATG	4320
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Db	4321	AACATTAACCTTATAAAGCTCCAGCAGGAAATGCTGTAATAGAAAGCTGTGTTAAGACAGC	4380
QY	4381	ATGGAGGCTAGCTTTCTTAACAGCTTACCTTCCATCATTAAGTACCTTCTTGCCCTTAGG	4440
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Db	4441	ACCTGCGGAATTCGGAACAAAGGCAATTCAGAAAAAGAGATTAATCTTCCAGAAAAAGTA	4500
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Db	4501	GTTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTTTGTGCTGCAAAAGTTTGAAGTGTG	4560
QY	4561	CAGATAGTCTTACCAAGTAAATAAAGAACCAAGAGTGAAGAGTCAATCCCTTTCTAAT	4620
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RESULT 3
AR033056
LOCUS AR033056 5711 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5869245.
ACCESSION AR033056
VERSION AR033056.1 GI:5948661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Yeung, A.T.
TITLE Mismatch endonuclease and its use in identifying mutations in targeted polynucleotide strands
JOURNAL Patent: US 5869245-A 1 09-FEB-1999;
FEATURES
source location/Qualifiers
BASE COUNT 1956 a 1099 c 1274 g 1382 t
ORIGIN
Query Match 100.0%; Score 5709.4; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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VERSION      U14680
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ORGANISM      Homo sapiens
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AUTHORS      Miki,Y., Swensen,J., Shattuck-Bidens,D., Futreal,P.A., Harselman,K.,
Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M., Ding,W., Bell,R.,
Rosenblatt,J., Hussey,C., Tran,T., McClure,M., Frye,C., Hattier,T.,
Phelps,R., Haugen-Strano,A., Katcher,H., Yakumo,K., Gholami,Z.,
Shaffer,D., Stone,S., Bayer,S., Way,C., Boden,R., Dayananth,P.,
Ward,J., Tonin,P., Narod,S., Bristow,P.K., Norris,F.H.,
Helvering,L., Morrison,P., Rostock,P., Lai,M., Barrett,J.C.,
Lewis,C., Neuhausen,S., Cannon-Albright,L., Goldgar,D., Wiseman,R.,
Kamb,A. and Skolnick,M.H.
A strong candidate for the breast and ovarian cancer susceptibility
gene BRCA1
JOURNAL      Science 266 (5182), 66-71 (1994)
MEDLINE      95025896

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PUBMED      7545954
REFERENCE      2 (bases 1 to 5711)
AUTHORS      Skolnick,M.H.
TITLE      Direct Submission
JOURNAL      Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and
the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City,
UT 84108, USA
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QY 2101 GGCACAGCAGAAACCTTACAACTCATGAAAGTAAAGAACTGCAACTGGAGCAGAGAAAG 2160
Db 2101 GGCACAGCAGAAACCTTACAACTCATGAAAGTAAAGAACTGCAACTGGAGCAGAGAAAG 2160
QY 2161 GTAACAGGCCAAATGAACAGCAATTAAGAAAGCAGAGAGTCTTTCCAGAGCGTGA 2220
Db 2161 GTAACAGGCCAAATGAACAGCAATTAAGAAAGCAGAGAGTCTTTCCAGAGCGTGA 2220
QY 2221 AGTTAACAAATGACACTGTTCTTTTACTTAAGTGTTCAAATACAGTGAACCTTAAGAAAT 2280
Db 2221 AGTTAACAAATGACACTGTTCTTTTACTTAAGTGTTCAAATACAGTGAACCTTAAGAAAT 2280
QY 2281 TTGTCAATCTTAGCTTCCAGAGAGAGAAAAAGAGAGAACTAGAAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTTAGCTTCCAGAGAGAGAAAAAGAGAGAACTAGAAAACAGTTAAAGTGT 2340

QY 2341 CTAATTAATGCTGAAGAGCCCCAAGATCTCATGTTAAGTGAAGAAAGGGTTTTCGCAACTG 2400
Db 2341 CTAATTAATGCTGAAGAGCCCCAAGATCTCATGTTAAGTGAAGAAAGGGTTTTCGCAACTG 2400
QY 2401 AAAGATCTGTAAGAGATGAGCAGTATTTTCAATGGTACTGTAAGTGAATGGAATGCAAG 2460
Db 2401 AAAGATCTGTAAGAGATGAGCAGTATTTTCAATGGTACTGTAAGTGAATGGAATGCAAG 2460
QY 2461 AAAGTATCTGTTACTGGAAGTTGCACTCTAGGGAAGGAAAAACGAACCAAAATTAAT 2520
Db 2461 AAAGTATCTGTTACTGGAAGTTGCACTCTAGGGAAGGAAAAACGAACCAAAATTAAT 2520
QY 2521 GTGTGAGTCAAGTGAAGCAATTTGAAAAACCCAAAGGACTAATTCATGTTGTTCCAAAG 2580
Db 2521 GTGTGAGTCAAGTGAAGCAATTTGAAAAACCCAAAGGACTAATTCATGTTGTTCCAAAG 2580
QY 2581 ATAAATAGAAATGACACAGAAAGCCTTTAAGTATTCATTGGGACATGAAGTTAACCAAGTC 2640
Db 2581 ATAAATAGAAATGACACAGAAAGCCTTTAAGTATTCATTGGGACATGAAGTTAACCAAGTC 2640
QY 2641 GGGAAACAGCAGATGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATCAT 2700
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QY 2701 TCAAGGTTTCAAAAGCGCAGTCAATTTGCTGTTTCAATTCAGAGAAATGCAAGAGAG 2760
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Db 2821 TTGAATGGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTCTAATATCAAGCTGTAC 2880
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QY 3301 TAGGTTCCAGTGAAGAAACATTCACAGAACTAGGTAAAGAAACAGAGGCGCAAAATTTGA 3360
Db 3301 TAGGTTCCAGTGAAGAAACATTCACAGAACTAGGTAAAGAAACAGAGGCGCAAAATTTGA 3360
QY 3361 ATGCTATGCTTAAGTTAGGGGTTTTGCAACCTGAGGCTTAATAACAAAGTCTTCCGAGAA 3420
Db 3361 ATGCTATGCTTAAGTTAGGGGTTTTGCAACCTGAGGCTTAATAACAAAGTCTTCCGAGAA 3420
QY 3421 GTAATTTGAACATCTGAAATAATAAGAAAGAAATATGAAGAAATGAGTTCAAGCTGTTA 3480

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Db      3481  ATACAGATTTCTGTCCATCTGATTTTCAATTAAGTATAGAACAGCCATAGGGAATAGTC 3540
QY      3541  ATGCATCTCAGGTTTGTCTGAGAACACTGATGACCTGTATGATGATGATGAATTAAG 3600
Db      3541  ATGCATCTCAGGTTTGTCTGAGAACACTGATGACCTGTATGATGATGATGAATTAAG 3600
QY      3601  AAGATCTAGTTTGTCTGAGAACACTGATGACCTGTATGATGATGATGAATTAAG 3660
Db      3601  AAGATCTAGTTTGTCTGAGAACACTGATGACCTGTATGATGATGATGAATTAAG 3660
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QY      3721  GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGAGGATG 3780
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Db      3781  AAGAGCTTCCCTGCTTCCAACTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
QY      3841  CTACTGTGGAGTATACCGCTGTGCTACCGAGTGTCTGCTAAGAACACAGAGGAAATTTAT 3900
Db      3841  CTACTGTGGAGTATACCGCTGTGCTACCGAGTGTCTGCTAAGAACACAGAGGAAATTTAT 3900
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Db      3901  TATCATTTGAAGATAGCTTAAATAGTACAGTAAACAGGTAATATTGGCAAGGATCTC 3960
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Db      3961  AGGAACATCACTTATGAGGAAACAAATGTTCTGCTAGCTTGTCTTCACTGCA 4020
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Db      4021  GTGAATTTGGAAGCTTGAAGTGAAGCAATTAACAACCCAGAGTCTCTTCTGATTTGTTCT 4080
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QY      4261  ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCACTCAGCAGAGGATACCATG 4320
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Db      4321  AACATTAACCTGATTAAGTTCAGCAGAGAAATGGCTGAACCTGATGAAGCTGTGAAG 4380
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Db      4381  ATGGAGCAGAGCTTGAACAGTACCTTCACTCAATTAAGTGAATTTTCTGCTTGAAG 4440
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Db      4501  GTGAATACCTTATAGCAGAAATCCAGAAAGCTTTCTGCTGAACAAGTTGAGGTCTG 4560
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Db      4561  CAGATAGTTCTACAGTAAATAAAGAACAGAGAGTGAAGGTCATCCCTCTTAAT 4620
QY      4621  GCCCATATTAGATGATAGTGTGATCAGAGTGTCTGTGAGTCTTCAAGATAGA 4680
Db      4621  GCCCATATTAGATGATAGTGTGATCAGAGTGTCTGTGAGTCTTCAAGATAGA 4680
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Db      4681  ACTACCATCTCAAGAGAGCTCTTAAGTGTGATGATGAGAGCAACAGCTGGAAG 4740
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Db      5221  TGAATATTTTCTAGGAATTCGCGAGAGAAATGGGTAGTATGCTATTTCTGGGTGACCC 5280
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Db      5281  AGCTATTAAGAAAGAAATGCTGAATGAGCAATGTTGAAGTCAAGAGAGATGTGG 5340
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Db      5341  TCAATGGAAGAAACCAAGAGTCCAAAGCGAGCAAGAGAAATCCAGAGCAAGAAAGAT 5400
QY      5401  TCAGGGGCTAGAAATCTGTGCTATGAGGCTCTTCAACAACATGCTCCACAGATCAATGG 5460
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Db      5461  AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
QY      5521  GCACAGGTGTCACCAATTTGTGTTGAGAGCCAGATGCTGAGCAGAGCAATGAGT 5580
Db      5521  GCACAGGTGTCACCAATTTGTGTTGAGAGCCAGATGCTGAGCAGAGCAATGAGT 5580
QY      5581  TCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTAACCCAGAGAGTGTGTGACA 5640
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QY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711
RESULT 5
AR070223 5712 bp DNA linear PAT 18-FEB-2000
LOCUS Sequence 1 from patent US 5891857.
DEFINITION AR070223
ACCESSION AR070223
VERSION AR070223.1 GI:7221111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,
Jelton,T.L., Robinson-Benion,C.L. and Thompson,M.E.
TITLE Characterized BRCA1 and BRCA2 proteins and screening and
JOURNAL therapeutic methods based on characterized BRCA1 and BRCA2 proteins
FEATURES
source 1. 5712
location/Qualifiers
BASE COUNT 1956 a 1099 c 1274 g 1383 t
ORIGIN
Query Match 100.0%; Score 5709.4; DB 6; Length 5712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGCTCGCTGAGACTTCTCTGACACCCGACACAGGCTGTGGGGTTTCTCAGATTAAGTGGGC 60
DB 1 AGCTCGCTGAGACTTCTCTGACACCCGACACAGGCTGTGGGGTTTCTCAGATTAAGTGGGC 60
QY 61 CTGCGCTCAGAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAA 120
DB 61 CTGCGCTCAGAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAA 120
QY 121 TGGATTTATCTGCTCTTGGCGGTGAAGAAGTACAAAGTCAATTAATGCTATGAGAGAAA 180
DB 121 TGGATTTATCTGCTCTTGGCGGTGAAGAAGTCAATTAATGCTATGAGAGAAA 180
QY 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGAACTGTCTCCAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGAACTGTCTCCAAAGTGTGACC 240
QY 241 ACATATTTTGGCAATTTTGCATGTGAAACCTTCTCAACCAAGAAAGGGCTTCAAGT 300
DB 241 ACATATTTTGGCAATTTTGCATGTGAAACCTTCTCAACCAAGAAAGGGCTTCAAGT 300
QY 301 GTCTTTATATGAAGATATATTAACCAAGAGGCTCAAGAAAGTACGAGATTAGTC 360
DB 301 GTCTTTATATGAAGATATATTAACCAAGAGGCTCAAGAAAGTACGAGATTAGTC 360
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DB 481 AAGTTTCTATCATCAAGATAGGGCTACAGAAACCGGCCAAAAGAGCTTCAAGAGTG 540
QY 541 AACCCGAAATCTTCTTGGCAGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600

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DB 601 CTGTAGAACCTCTGAGACCAAGACGGGATACCACTCAAAAGAGCTCTGTACTACTTG 660
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Dh 1921 ACAATTCAAAAGCAGCTTAAAGAAATAGGCTGAGAGAGAAAGTCTTACAGGAGATTC 1980
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Dh 3181 GTACAGTGAACAATTAAGCCTGAATTAACATTTAGAGAAAATGTTTAAAGAGCAGCT 3240
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Dh 3241 CAGCAATTTAATGAAGTGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAAG 3300
Qy 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGAGAACTAGTGAAGAAAGAGGCGCAAAATGA 3360
Dh 3301 TAGGTTCCAGTATGAAGAAACATTCAGAGAGAACTAGTGAAGAAAGAGGCGCAAAATGA 3360
Qy 3361 ATGCTATGCTTATGATTAAGAGGTTTGCAGACCTGAGGCTATTAACAAAGCTTCTCTGGA 3420
Dh 3361 ATGCTATGCTTATGATTAAGAGGTTTGCAGACCTGAGGCTATTAACAAAGCTTCTCTGGA 3420
Qy 3421 GTAAATGTGAAGATCTGAATTAAGAAAGCAAGAAATGAAGAGTGAAGTGAAGTGAAG 3480
Dh 3421 GTAAATGTGAAGATCTGAATTAAGAAAGCAAGAAATGAAGAGTGAAGTGAAGTGAAG 3480
Qy 3481 ATACAGATTTCTCTCATATCTGATGATGATGATGATGATGATGATGATGATGATGATG 3540
Dh 3481 ATACAGATTTCTCTCATATCTGATGATGATGATGATGATGATGATGATGATGATGATG 3540
Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGATGATGATGATG 3600
Dh 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGATGATGATGATG 3600
Qy 3601 AAAGATCTAGTGTGCTGAAGAAATGACATTAAGAAAGTGTGCTGTTTGAAGAAAGG 3660
Dh 3601 AAAGATCTAGTGTGCTGAAGAAATGACATTAAGAAAGTGTGCTGTTTGAAGAAAGG 3660
Qy 3661 TCCAGAAAGAGAGTTGAGCAGAGTCTAGGCTTTACACCATACACATTTGGCTCAGG 3720
Dh 3661 TCCAGAAAGAGAGTTGAGCAGAGTCTAGGCTTTACACCATACACATTTGGCTCAGG 3720
Qy 3721 GTTACCGAAGAGGCGCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTGAAGTGA 3780
Dh 3721 GTTACCGAAGAGGCGCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTGAAGTGA 3780
Qy 3781 AAGAGCTTCCCTGCTTCAACACTTGTATTTGTGAAGTAAACATATACCTTCTCAGT 3840
Dh 3781 AAGAGCTTCCCTGCTTCAACACTTGTATTTGTGAAGTAAACATATACCTTCTCAGT 3840

source	1. .5712	/organism="unknown"
BASE COUNT	1956 a	1099 c 1274 g 1383 t
ORIGIN		

Query Match 100.0%; Score 5709.4; DB 6; Length 5712;

QY	1	AGCTGCTGAGACTTCCTGCGAACCCCGACACAGGCTGTGGGGTTTCTCAATATACATGAGGC	60
Db	1	AGCTGCTGAGACTTCCTGCGAACCCCGACACAGGCTGTGGGGTTTCTCAATATACATGAGGC	60
QY	61	CCTGGCCTCAGAGAGGCTTCAACCTCTGCTCTGGTAAAGTTTCATTGGAACAGAAAGAA	120
Db	61	CCTGGCCTCAGAGAGGCTTCAACCTCTGCTCTGGTAAAGTTTCATTGGAACAGAAAGAA	120
QY	121	TGATATTATCTGCTCTTGGCGTTGAAGAGTACAAAATGTCAATTATGCTATGACAGAAA	180
Db	121	TGATATTATCTGCTCTTGGCGTTGAAGAGTACAAAATGTCAATTATGCTATGACAGAAA	180
QY	181	TCTTAGAGTGCCTTCCTGCGAGTTGATATCAAGGAACCTGTCTCCAAAGTGTGACC	240
Db	181	TCTTAGAGTGCCTTCCTGCGAGTTGATATCAAGGAACCTGTCTCCAAAGTGTGACC	240
QY	241	ACATATTTTGGCAATTTTTCATGCTGAAACCTTCTCAACGAGAGAAAGAGGCTTCAAGT	300
Db	241	ACATATTTTGGCAATTTTTCATGCTGAAACCTTCTCAACGAGAGAAAGAGGCTTCAAGT	300
QY	301	GTCCTTTATGTAGAATGATATATACCAAAAGAGCCTACAAAGAAAGTACAGATTTAGTC	360
Db	301	GTCCTTTATGTAGAATGATATATACCAAAAGAGCCTACAAAGAAAGTACAGATTTAGTC	360
QY	361	AACTTGTGAAGAGCTATTTGAATAATCATTTTGTGCTTTTACGCTTGCACAGTTTGGAGT	420
Db	361	AACTTGTGAAGAGCTATTTGAATAATCATTTTGTGCTTTTACGCTTGCACAGTTTGGAGT	420
QY	421	ATGCAAAACAGCTATTAATTTTGGCAAAAAGAGAAATATACCTCTCTGAAACATCTTAAAGATG	480
Db	421	ATGCAAAACAGCTATTAATTTTGGCAAAAAGAGAAATATACCTCTCTGAAACATCTTAAAGATG	480
QY	481	AAAGTTCTATCATCCAAAGATATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG	540
Db	481	AAAGTTCTATCATCCAAAGATATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG	540
QY	541	AAACCGGAAATCTCTTCCTTTCGACGAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGGA	600
Db	541	AAACCGGAAATCTCTTCCTTTCGACGAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGGA	600
QY	601	CTGTGAGAACTCTGTGAGCAAAAGCAGCGGATACAACTCCAAAGACGTGTGACTCATTG	660
Db	601	CTGTGAGAACTCTGTGAGCAAAAGCAGCGGATACAACTCCAAAGACGTGTGTCTACATTG	660
QY	661	AATTGGATCTGATTCCTTCTGAAGATACCGTTAATTAAGGCACTTAATTGCAGTGTGGAG	720
Db	661	AATTGGATCTGATTCCTTCTGAAGATACCGTTAATTAAGGCACTTAATTGCAGTGTGGAG	720
QY	721	ATCAAGAATTTGTTACAATCACCCCTCAAGGAACCAAGGATATAATCAGTTTGGATTCTG	780
Db	721	ATCAAGAATTTGTTACAATCACCCCTCAAGGAACCAAGGATATAATCAGTTTGGATTCTG	780
QY	781	CAAAAAAGGCTGCTGTGATTTTCTGAGACGGATGTAAACAATATCTGAACATCATCAAC	840
Db	781	CAAAAAAGGCTGCTGTGATTTTCTGAGACGGATGTAAACAATATCTGAACATCATCAAC	840
QY	841	CCAGTATATATGATTTTGAACACCACTGAGAAACGCTGACGCTGAGAGGCACTCCAGAAAT	900
Db	841	CCAGTATATATGATTTTGAACACCACTGAGAAACGCTGACGCTGAGAGGCACTCCAGAAAT	900
QY	901	ATCAGGGTATGTTCTGTTCCAACTTGCAATGTGAGCATGTGGCACAAATCTCATGCCA	960
Db	901	ATCAGGGTATGTTCTGTTCCAACTTGCAATGTGAGCATGTGGCACAAATCTCATGCCA	960

QY	961	UCTCATTTACAGCATGAGAACAGCGAGTTTATTATCTCACTAAAGACAGAAATGATAGATA	1020
Db	961	GCTATTACAGACAGAGAAACAGCGATTATTATCTCACTAAAGACAGAAATGATAGATA	1020
QY	1021	AGGCTGAATTCGTATATTAAGACAAACAGCTGGCTTAGCAGGAGCCAACTATAACGAT	1080
Db	1021	AGGCTGAATTCGTATATTAAGACAAACAGCTGGCTTAGCAGGAGCCAACTATAACGAT	1080
QY	1081	GGGCTGGAAGTAAGAAAACATGTAATGATAGCGGAGCTCCAGCAGCAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGAAAACATGTAATGATAGCGGAGCTCCAGCAGCAAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCCCTGTGTAGAGAAAAGAAATGGAATTAACAGAAATCGCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCCCTGTGTAGAGAAAAGAAATGGAATTAACAGAAATCGCATGCT	1200
QY	1201	CAGAGAAATCCTAGAGATACCTGAAGATGTCCTTGATTAACCTAAATAGCAGATTGAGA	1260
Db	1201	CAGAGAAATCCTAGAGATACCTGAAGATGTCCTTGATTAACCTAAATAGCAGATTGAGA	1260
QY	1261	AAGTTAAATGAAGTGGTTTTCCAGAAAGTATGAACCTGTTAGGTTCTGAAGCTCACATGATG	1320
Db	1261	AAGTTAAATGAAGTGGTTTTCCAGAAAGTATGAACCTGTTAGGTTCTGAAGCTCACATGATG	1320
QY	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATTGACGTTCTAATAGAGGTAGATG	1380
Db	1321	GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATTGACGTTCTAATAGAGGTAGATG	1380
QY	1381	AATTTCTGGTCTTCAGAGAAAATATACTTACTGGCAGATGATCCCATAGAGGCTTTAA	1440
Db	1381	AATTTCTGGTCTTCAGAGAAAATATACTTACTGGCAGATGATCCCATAGAGGCTTTAA	1440
QY	1441	TATGTAAAGTGAAAGAGTTCACTCCAAATCAGTAGAGAGATAATTGAAGACAAAATAT	1500
Db	1441	TATGTAAAGTGAAAGAGTTCACTCCAAATCAGTAGAGAGATAATTGAAGACAAAATAT	1500
QY	1501	TTGGGAAAACCTATCGAGAAAGGACAGCTCCCAACCTTAAGCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACCTATCGAGAAAGGACAGCTCCCAACCTTAAGCATGTAACTGAAAATC	1560
QY	1561	TAAATTATAGAGCATTTTGTTACTGAGGCCACAGATTAATACAAGAGCCCTCCACAAATA	1620
Db	1561	TAAATTATAGAGCATTTTGTTACTGAGGCCACAGATTAATACAAGAGCCCTCCACAAATA	1620
QY	1621	AATTTAAAGCGTAAAAGGAGACCTPACATCAGAGCCCTTACTCTGAGAGATTTTATCAAGAAG	1680
Db	1621	AATTTAAAGCGTAAAAGGAGACCTPACATCAGAGCCCTTACTCTGAGAGATTTTATCAAGAAG	1680
QY	1681	CAGATTTGGCAGTTCAAAAGACTCTCTGAAAATGATAAATCAGGGAACTTAACCAACGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTCTGAAAATGATAAATCAGGGAACTTAACCAACGAGC	1740
QY	1741	AGAAATGGTCAAGTATGAATATTAATTAATGTGTCTATGGAATTAACAAAGAGTGATTT	1800
Db	1741	AGAAATGGTCAAGTATGAATATTAATTAATGTGTCTATGGAATTAACAAAGAGTGATTT	1800
QY	1801	CTATTTCGAATGAGAAAATCCTTAACCCATAGAAATACATCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTTCGAATGAGAAAATCCTTAACCCATAGAAATACATCGAAAAAGAAATCTGCTTTCA	1860
QY	1861	AAACGAAGCTGAAACCTATTAAGCAGCAGTATAAGCAATATAGAACTCGAATTTAAATATCC	1920
Db	1861	AAACGAAGCTGAAACCTATTAAGCAGCAGTATAAGCAATATAGAACTCGAATTTAAATATCC	1920
QY	1921	ACAAATTCAAAAGCACTTAATAAGATATGGCTGAGAGAAAGCTTTCTACAGCATATTC	1980
Db	1921	ACAAATTCAAAAGCACTTAATAAGATATGGCTGAGAGAAAGCTTTCTACAGCATATTC	1980
QY	1981	ATGGGCTTGAACATAGTATGACAGTAGAAATCTAAGCCCACTAATTGATCGAATTTGCAAA	2040
Db	1981	ATGGGCTTGAACATAGTATGACAGTAGAAATCTAAGCCCACTAATTGATCGAATTTGCAAA	2040
QY	2041	TTGATATGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACCAACCAATCCAGTCA	2100

Db 2041 TTGATAGTGTCTTCTGAGTGAAGATTAAGAAAAAGTACACAAATGCCAGTCA 2100
Qy 2101 GGCACAGAGAAACCTTCAACTCATGAGAAAGTAAAGAACTTGCACCTGAGCAAGAGA 2160
Db 2101 GGCACAGAGAAACCTTCAACTCATGAGAAAGTAAAGAACTTGCACCTGAGCAAGAGA 2160
Qy 2161 GTAACAGCCAAATGAAGACAACTAAAGACATGACGAGATCTTTCCAGAGCTGA 2220
Db 2161 GTAACAGCCAAATGAAGACAACTAAAGACATGACGAGATCTTTCCAGAGCTGA 2220
Qy 2221 AGTTAACAAATGACACCTGCTCTTTTACTAAGTGTCAATATCAGTGAACCTTAAAGAT 2280
Db 2221 AGTTAACAAATGACACCTGCTCTTTTACTAAGTGTCAATATCAGTGAACCTTAAAGAT 2280
Qy 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAACTTGAACATGTTAAAGTGT 2340
Db 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAACTTGAACATGTTAAAGTGT 2340
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTATGTTAAGTGAAGAAAGGTTTGCACAACTG 2400
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTATGTTAAGTGAAGAAAGGTTTGCACAACTG 2400
Qy 2401 AAAGATCTGTAGAGTAGACATATTTCAATGTAACCTGTACTGATTAATGACACTCAG 2460
Db 2401 AAAGATCTGTAGAGTAGACATATTTCAATGTAACCTGTACTGATTAATGACACTCAG 2460
Qy 2461 AAAGATCTGTACTGTAGAGTAGACATCTTGAAGAGGCAAAACAGAACCAATTAAT 2520
Db 2461 AAAGATCTGTACTGTAGAGTAGACATCTTGAAGAGGCAAAACAGAACCAATTAAT 2520
Qy 2521 GTGTAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGAACTAATTCATGTTGTTCCAAAG 2580
Db 2521 GTGTAGTCAAGTGTGACAGATTTGAAAAACCCCAAGGAACTAATTCATGTTGTTCCAAAG 2580
Qy 2581 ATAAATAGAAATGACACAGAGGCTTAAAGTATCAATGGACATGAAGTTAAACAAGTGC 2640
Db 2581 ATAAATAGAAATGACACAGAGGCTTAAAGTATCAATGGACATGAAGTTAAACAAGTGC 2640
Qy 2641 GGGAAACAGACATAGAAATGAGAAAGTGAACCTTGAATCTCAGATTTGCGAATATCACT 2700
Db 2641 GGGAAACAGACATAGAAATGAGAAAGTGAACCTTGAATCTCAGATTTGCGAATATCACT 2700
Qy 2701 TCAAGGTTTCAAAAGGCGCAGTCAATTTGCTCTGTTTCAAAATCAGGAAATGCGAAGAGG 2760
Db 2701 TCAAGGTTTCAAAAGGCGCAGTCAATTTGCTCTGTTTCAAAATCAGGAAATGCGAAGAGG 2760
Qy 2761 AATGTGCAACATTTCTGTGCCCACTGTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGTGCCCACTGTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGATGATCTAATCAAGCCTGTATC 2880
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGATGATCTAATCAAGCCTGTATC 2880
Qy 2881 AGACAGTTAATATCACTGACAGGCTTCTGTGTGTGTGATCAATCTCAGTTCAAGAGCA 2940
Db 2881 AGACAGTTAATATCACTGACAGGCTTCTGTGTGTGTGATCAATCTCAGTTCAAGAGCA 2940
Qy 2941 ATGCCAAATGTATATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000
Db 2941 ATGCCAAATGTATATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000
Qy 3001 ACGAAACGTGACTCTATCTCAATTAACATGAGCTTTTACAAAACCATATCGTATAC 3060
Db 3001 ACGAAACGTGACTCTATCTCAATTAACATGAGCTTTTACAAAACCATATCGTATAC 3060
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAGAAAAATCTGTGAGAG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAGAAAAATCTGTGAGAG 3120
Qy 3121 AAAAATTGAGAACATTCATATGTCACTGAAAGAGAAATGGAAATGGAACATTTCCAA 3180
Db 3121 AAAAATTGAGAACATTCATATGTCACTGAAAGAGAAATGGAAATGGAACATTTCCAA 3180

Db 3121 AAAAATTGAGAACATTCATATGTCACTGAAAGAGAAATGGAAATGGAACATTTCCAA 3180
Qy 3181 GTACAGTAGACACAATTAAGCCGTAAATACTTAAAGAAATGTTTAAAGAACCGACCT 3240
Db 3181 GTACAGTAGACACAATTAAGCCGTAAATACTTAAAGAAATGTTTAAAGAACCGACCT 3240
Qy 3241 CAAGCAATTAATGAAGTAGTTCACAGTAAATGAAGGAGGCTCCAGTATTAATGA 3300
Db 3241 CAAGCAATTAATGAAGTAGTTCACAGTAAATGAAGGAGGCTCCAGTATTAATGA 3300
Qy 3301 TAGGTTCCAGTAGAAGAAACATTCAGACAGAACTAGTAGAAACAGAGGCCCAAAATGA 3360
Db 3301 TAGGTTCCAGTAGAAGAAACATTCAGACAGAACTAGTAGAAACAGAGGCCCAAAATGA 3360
Qy 3361 TAGGTTCCAGTAGAAGAAACATTCAGACAGAACTAGTAGAAACAGAGGCCCAAAATGA 3420
Db 3361 TAGGTTCCAGTAGAAGAAACATTCAGACAGAACTAGTAGAAACAGAGGCCCAAAATGA 3420
Qy 3421 ATGCTATGCTTAAAGTAAAGGAGGTTTGAACCTGAGGCTTAAACAAAGTCTTCCAGAA 3480
Db 3421 ATGCTATGCTTAAAGTAAAGGAGGTTTGAACCTGAGGCTTAAACAAAGTCTTCCAGAA 3480
Qy 3481 GTAAATGTGAACATCTGAAATTAAGAAAGAGAAATGAAGAGTATGAGACTGTGA 3540
Db 3481 GTAAATGTGAACATCTGAAATTAAGAAAGAGAAATGAAGAGTATGAGACTGTGA 3540
Qy 3541 ATACAGATTTCTTCCATATCTGATTTTCAATTAATTAAGAAACAGCTTATGGAAGTATC 3600
Db 3541 ATACAGATTTCTTCCATATCTGATTTTCAATTAATTAAGAAACAGCTTATGGAAGTATC 3600
Qy 3601 AAGATCTAGTGTGCTGAAATATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3660
Db 3601 AAGATCTAGTGTGCTGAAATATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3660
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Db 3661 AAGATCTAGTGTGCTGAAATATGACATTAAGAAAGTGTGCTGTTTAAAGCAAAAGCG 3720
Qy 3721 TCCAGAAAGGAGCTTATGACAGAGGCTCTGACCTTTACCCATACATTTGGCTCAGG 3780
Db 3721 TCCAGAAAGGAGCTTATGACAGAGGCTCTGACCTTTACCCATACATTTGGCTCAGG 3780
Qy 3781 GTTACCGAAGAGGAGGCGCAAGAAATTAAGAGTCTCAGAAAGAACTTACTAGTAGAGATG 3840
Db 3781 GTTACCGAAGAGGAGGCGCAAGAAATTAAGAGTCTCAGAAAGAACTTACTAGTAGAGATG 3840
Qy 3841 AAGAGCTTCCCTGCTTCAACACTTGTATTTGTTGTAAGTAAACAATATACCTTCTCAGT 3900
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Db 3901 TATCATTGAAGAAATAGCTTAAATGATGCTGAGTAAACAGATTAATGGCAAGGATCTTC 3960
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Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGTAGCTGTTTCTTCAAGTGA 4020
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Db 4081 CCAACAAATAGGATCAGTCTGAAGCCAGGAGTGTGCTGAGAGCAAGAAATGG 4140
Qy 4141 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200
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Qy 4201 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4260
Db 4201 TTTGAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4260

OY	4261	ACTGCTCAGGGGTATCCCTCTCAGAGTGCATTTTAAACACTCAGACGAGGGATACCAAGC	4332
Db	4261	ACTGCTCAGGGGTATCCCTCTCAGAGTGCATTTTAAACACTCAGACGAGGGATACCAAGC	4320
OY	4321	AAACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGGCTGAACTAGAGACTCTGTTAGAACAGC	4380
Db	4321	AAACATTAACCTGATTAAGAGCTCCAGCAGAGAAATGGCTGAACTAGAGACTCTGTTAGAACAGC	4380
OY	4381	ATGGAGAGCCAGCTTCTTAACAGCTACCCCTTCATATTAAGTGAAGCTCTTGCCCTTGAAG	4440
Db	4381	ATGGAGAGCCAGCTTCTTAACAGCTACCCCTTCATATTAAGTGAAGCTCTTGCCCTTGAAG	4440
OY	4441	ACCTGCGAAATCCAGAACAAAGCACAATCAGAGAAAAAGCGTAACTTACACAGAAAAATA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCACAATCAGAGAAAAAGCGTAACTTACACAGAAAAATA	4500
OY	4501	GTTAAATACCTTATTAAGCCAGATCCAGAAAGCCCTTCTGCTGACAAAGTTTAGAGTGTG	4560
Db	4501	GTTAAATACCTTATTAAGCCAGATCCAGAAAGCCCTTCTGCTGACAAAGTTTAGAGTGTG	4560
OY	4561	CAGATAGTTCCTACCGATTAATAAAGAACAGAGGTGAAAGGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCCTACCGATTAATAAAGAACAGAGGTGAAAGGTCAATCCCTCTTAAT	4620
OY	4621	GCCCATCATTTGATATATAGTGTGCATAGCAGATGCTCTGGAGTCTTCAGAAATGA	4680
Db	4621	GCCCATCATTTGATATATAGTGTGCATAGCAGATGCTCTGGAGTCTTCAGAAATGA	4680
OY	4681	ACTACCCATCTCAGAGAGGCTCATTAAGTGTGATGATGGAGAGCAACAGCTGAG	4740
Db	4681	ACTACCCATCTCAGAGAGGCTCATTAAGTGTGATGATGGAGAGCAACAGCTGAG	4740
OY	4741	AGTCTGGGCGACACGATTTTGACGGAAACATCTTACTTGCCAAAGCAGATCTAAGGGAA	4800
Db	4741	AGTCTGGGCGACACGATTTTGACGGAAACATCTTACTTGCCAAAGCAGATCTAAGGGAA	4800
OY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGAGACCCCTGAATCTGATCCTTCTG	4860
Db	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTTCTCTGATGAGACCCCTGAATCTGATCCTTCTG	4860
OY	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACATCTTCAACCTTCGATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACATCTTCAACCTTCGATTTGA	4920
OY	4921	AAGTTCGCCAATTTGAAGTTTGACAAATCTGCCAGAGTCCAGCTGTGCTCATACTACTG	4980
Db	4921	AAGTTCGCCAATTTGAAGTTTGACAAATCTGCCAGAGTCCAGCTGTGCTCATACTACTG	4980
OY	4981	ATACTGCTGGGATTAATGCAATGGAAGAAAGTGAGAGGAGGAGAGCAAAATTTGACAG	5040
Db	4981	ATACTGCTGGGATTAATGCAATGGAAGAAAGTGAGAGGAGGAGAGCAAAATTTGACAG	5040
OY	5041	CTTCAACAGAAAGGGCTCAACAAAGAAATGTCATGTGTGTCTGTGCTGACCCACAGAG	5100
Db	5041	CTTCAACAGAAAGGGCTCAACAAAGAAATGTCATGTGTGTGTGTGCTGACCCACAGAG	5100
OY	5101	AATTTATGCTGTGTACAAAGTTTGCCAGAAAAACACACATCTTAACCTTAATCTTAATTA	5160
Db	5101	AATTTATGCTGTGTACAAAGTTTGCCAGAAAAACACACATCTTAACCTTAATCTTAATTA	5160
OY	5161	CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGATTTGTGTGTGAACGGACAC	5220
Db	5161	CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGATTTGTGTGTGAACGGACAC	5220
OY	5221	TGAAATATTTCTAGAGAAATGCGAGGAGAAATGGTATGATAGCTATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTCTAGAGAAATGCGAGGAGAAATGGTATGATAGCTATTTCTGGGTGACCC	5280
OY	5281	AGTCATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAAATGTGG	5340
Db	5281	AGTCATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAAATGTGG	5340

Oy		5341	TCATGTGAAAGAACCAACCAAGCTCCAAAGCAGACAAGAGTCCAGACAGAAAGACT	5400
Dd		5341	TCATGTGAAAGAACCAACCAAGCTCCAAAGCAGACAAGAGTCCAGACAGAAAGACT	5400
Oy		5401	TCAGGGGGCTGAATACTGTGTGCTAATGAGGCCCTTACCACCATGCACAGATCAACTCG	5468
Dd		5401	TCAGGGGGCTGAATACTGTGTGCTAATGAGGCCCTTACCACCATGCACAGATCAACTCG	5468
Oy		5461	AATGATGTGTACAGCTGTGTGTCTTTCTGTGTGAAGAAGAGCTTTATCATTCACCTTG	5520
Dd		5461	AATGATGTGTACAGCTGTGTGTCTTTCTGTGTGAAGAAGAGCTTTATCATTCACCTTG	5520
Oy		5521	GCAACAGGTGTCCACCCAAATTGTGTGTGTGACGCCAGATTCGCTGTGACAGAGACAATGGCT	5580
Dd		5521	GCAACAGGTGTCCACCCAAATTGTGTGTGTGACGCCAGATTCGCTGTGACAGAGACAATGGCT	5580
Oy		5581	TCCATGTCAATTTGGGACAGATGTGTAGGACACCTGTGTGTGACCCGAGATGGGTGTGGACA	5640
Dd		5581	TCCATGTCAATTTGGGACAGATGTGTAGGACACCTGTGTGTGACCCGAGATGGGTGTGGACA	5640
Oy		5641	GTGTAGCACCTGTACAGTCCAGTCCGAGAGCTGTGACACCTTAACCTGATACCCCAGATCCCCACA	5700
Dd		5641	GTGTAGCACCTGTACAGTCCAGTCCGAGAGCTGTGACACCTTAACCTGATACCCCAGATCCCCACA	5700
Oy		5701	GCACACTACTGA 5711	
Dd		5701	GCACACTACTGA 5711	
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AR125601	LOCUS	AR125601	5712 bp	DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 1 from patent US 6177410.			
ACCESSION	AR125601			
VERSION	AR125601.1 GI:14111663			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 5712)			
AUTHORS	Holt J.T., Jensen R.A., King M.-C., Steiner M.S., Robinson-Benton C.L. and Thompson M.E.			
TITLE	Therapeutic methods for prostate cancer			
JOURNAL	Patent: US 6177410-A 1 23-JAN-2001;			
FEATURES	Location/Qualifiers			
source	1..5712			
BASE COUNT	1956 a 1099 c 1274 g 1383 t			
ORIGIN	/organism="unknown"			
<hr/>				
Query Match	100.0%; Score 5709.4; DB 6; Length 5712;			
Best Local Similarity	100.0%; Pred. No. 0;			
Matches 5710; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
Oy		1	AGCTCGCTGAGACTTCTCTGGAACCCCGACACAGGCTGTGGGGTTTCTCAGATAACTGCGCC	60
Dd		1	AGCTCGCTGAGACTTCTCTGGAACCCCGACACAGGCTGTGGGGTTTCTCAGATAACTGCGCC	60
Oy		61	CTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAAGAA	120
Dd		61	CTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAAGAA	120
Oy		121	TGAGATTATCTGCTCTCGCGGTTGAAGAAGTACAAAATGTCATTAAATGCTATGACAGAAA	180
Dd		121	TGAGATTATCTGCTCTCGCGGTTGAAGAAGTACAAAATGTCATTAAATGCTATGACAGAAA	180
Oy		181	TCTTAGAGTGTCCCATCTGTCTGGAAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC	240
Dd		181	TCTTAGAGTGTCCCATCTGTCTGGAAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC	240
Oy		241	ACATATTTTGCMAATTTTGTGATGTGAAACTTTCAACCAAGAAAGGGCTTTCACAGT	300
Dd		241	ACATATTTTGCMAATTTTGTGATGTGAAACTTTCAACCAAGAAAGGGCTTTCACAGT	300

QY 301 GTCCTTATGTAAAGATATATTAACCAAGAGGCTCAAGAAAGTACGAGATTATGTC 360
Db 301 GTCCCTTATGTAAAGATATATTAACCAAGAGGCTCAAGAAAGTACGAGATTATGTC 360
QY 361 AACTTGTGAAGAGCTATTTGAAMAATCATTTGTGCTTTTCAGCTTGACACAGGTTTGAAT 420
Db 361 AACTTGTGAAGAGCTATTTGAAMAATCATTTGTGCTTTTCAGCTTGACACAGGTTTGAAT 420
QY 421 ATGCAACAGCTATTAATTTTGGCAAAAAAGAAATTAATCTCTGTAACATCTTAAAGATG 480
Db 421 ATGCAACAGCTATTAATTTTGGCAAAAAAGAAATTAATCTCTGTAACATCTTAAAGATG 480
QY 481 AAGTTTCATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGAGACTTCTACAGAGTG 540
Db 481 AAGTTTCATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGAGACTTCTACAGAGTG 540
QY 541 AACCAGAAATCCTTCTCTTGAGGAAACCAAGTCTGAGTGTCCAACTCTCTAACTTTGAA 600
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QY 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGATCAAACTCAAAAGAGCTCTGTCTACATTTG 660
Db 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGATCAAACTCAAAAGAGCTCTGTCTACATTTG 660
QY 661 AATTGGGATCTGATTTCTGAGAGATACCGTTAATAGGCACTTAATGCAAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTGAGAGATACCGTTAATAGGCACTTAATGCAAGTGTGGAG 720
QY 721 ATCAAGATTTGTACAAATCAACCCCTCAAGGAAACAGGAGTGAATCAAGTTGATTTCTG 780
Db 721 ATCAAGATTTGTACAAATCAACCCCTCAAGGAAACAGGAGTGAATCAAGTTGATTTCTG 780
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGAACAAATCTGAACATCTCATCAC 840
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGAACAAATCTGAACATCTCATCAC 840
QY 841 CCAGTAAATATGATTTTGAACACCACTGAGAAAGCTGAGAGGCTCAGAAAAAGT 900
Db 841 CCAGTAAATATGATTTTGAACACCACTGAGAAAGCTGAGAGGCTCAGAAAAAGT 900
QY 901 ATCAGGAGTGTCTGTTCAAACCTTGATGAGGACCATGTGGCACAAAATCTCATGCCA 960
Db 901 ATCAGGAGTGTCTGTTCAAACCTTGATGAGGACCATGTGGCACAAAATCTCATGCCA 960
QY 961 GCTCATTAACAGATGAGAAACAGCACTTTATTACTCACTAAGACAGAAATGATGAAA 1020
Db 961 GCTCATTAACAGATGAGAAACAGCACTTTATTACTCACTAAGACAGAAATGATGAAA 1020
QY 1021 AGGCTGAATTTCTGTAAATAAAGCAAAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080
Db 1021 AGGCTGAATTTCTGTAAATAAAGCAAAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAGGAAAATGATTAATGATGAGCGGACCTCCAGCAAGAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTAAGGAAAATGATTAATGATGAGCGGACCTCCAGCAAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAAAACCTGCAATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAAAACCTGCAATGCT 1200
QY 1201 CAGAGAAATCTAGAGATCTGAAGATGTTCTTGTGATAACAATAATAGCAGATTTGACA 1260
Db 1201 CAGAGAAATCTAGAGATCTGAAGATGTTCTTGTGATAACAATAATAGCAGATTTGACA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATCTGTAGGTTCTGATGAATCAATGATG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATCTGTAGGTTCTGATGAATCAATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGACGTTCTAAATGAGGTAGTG 1380
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGACGTTCTAAATGAGGTAGTG 1380

QY 1381 AATAATTCGTGTTCTTACAGAAATAATAGACTTACTGCGCAGATGATCCTCATAGGCTTTAA 1440
Db 1381 AATAATTCGTGTTCTTACAGAAATAATAGACTTACTGCGCAGATGATCCTCATAGGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTTCATCTCAATCAGTAGAGATATATTTGAACAAATAT 1500
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QY 1501 TTGGGAAACCTATCGGAAGAGGACCGCTCCCACTTAAGCATGTAAGTGAATATC 1560
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Db 1621 AATTAAACGTTAAAGAGACCTTACATGAGGCTTCACTCTGAGATTTTATCAAGAA 1680
QY 1681 CAGATTTGGGAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC 1740
Db 1681 CAGATTTGGGAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC 1740
QY 1741 AGAATGTCAGATGATTAATTAATTAATAGTGTCTACAGAAATCAAAAGTGATTT 1800
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Db 1801 CTATTCAGATGAGAAAAATCTTAAACCAATAGATCACTGAAAAAGAAATCTGCTTTCA 1860
QY 1861 AAAAGAAAGCTGAACCTATTAAGAGAGCTATTAAGCAATATGAACTGAATTAATATCC 1920
Db 1861 AAAAGAAAGCTGAACCTATTAAGAGAGCTATTAAGCAATATGAACTGAATTAATATCC 1920
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Db 1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAAAGTCTTACAGGACATATTC 1980
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Db 2101 GGCAACAGCAAAACCTCAACTCATGGAAGTAAAGAACTGCAATGAGCCAGAAAGA 2160
QY 2161 GTAAACAGCCAAATGAACAGCAAGTAAAGACATGACACGATACCTTCCAGAGCTGA 2220
Db 2161 GTAAACAGCCAAATGAACAGCAAGTAAAGACATGACACGATACCTTCCAGAGCTGA 2220
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QY 2281 TTGTCAATCCTAGCCTTCCAAAGAGAAAGAAAGAAAGTAAAGAGTGT 2340
Db 2281 TTGTCAATCCTAGCCTTCCAAAGAGAAAGAAAGAAAGTAAAGAGTGT 2340
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Db 2341 CTAAATTAATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGGTTTGCAAACTG 2400
QY 2401 AAAAGTCTGTAGAGTAGAGATTTTCAATGAGTCTGATGATTTATGAGCACTCAGG 2460
Db 2401 AAAAGTCTGTAGAGTAGAGATTTTCAATGAGTCTGATGATTTATGAGCACTCAGG 2460
QY 2461 AAGATATCTGTTACTGGAAGTTAGCACTTAGGAAAGGCAAAACAGAACTAAATTAAT 2520

D	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTTGAAGGAGCAAAAACAGAACCAATAAT	2520
Q	2521	GTGTGAGTCAGTGTGACGACATTTGAAAACCCCAAGGACATAATTGATGTTTCCAAG	2580
D	2521	GTGTGAGTCAGTGTGACGACATTTGAAAACCCCAAGGACATAATTGATGTTTCCAAG	2580
Q	2581	ATATAATGAATACACAGAAAGCTTAAAGTATCCATTGGGACATGAAGTTAACACAGCTC	2640
D	2581	ATATAATGAATACACAGAAAGCTTAAAGTATCCATTGGGACATGAAGTTAACACAGCTC	2640
Q	2641	GGGAAACAAAGCATAGAAAATGSAAGAAAGTAACTGATGCTCAGTATTTGCGAATACAT	2700
D	2641	GGGAAACAAAGCATAGAAAATGSAAGAAAGTAACTGATGCTCAGTATTTGCGAATACAT	2700
Q	2701	TCGAAGTTTCAAAAGGCCAGTCATTTGCTGTGTTTCAAAATCAGAAATGACAGAAAGG	2760
D	2701	TCGAAGTTTCAAAAGGCCAGTCATTTGCTGTGTTTCAAAATCAGAAATGACAGAAAGG	2760
Q	2761	AATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAACAAAGTCCAAAGTCACTT	2820
D	2761	AATGTGCAACATTTCTCTGCCACTCTGGGTCTTAAAGAACAAAGTCCAAAGTCACTT	2820
Q	2821	TTGAATGTGAACAAAAGGAGAAATCAAGSAAATGAGCTATATCAAGCCTGTAC	2880
D	2821	TTGAATGTGAACAAAAGGAGAAATCAAGSAAATGAGCTATATCAAGCCTGTAC	2880
Q	2881	AGACAGTTAATATCACTGACAGCTTCTGTGTGTGTGTCAGAAAGATTAAGCAGTTGATA	2940
D	2881	AGACAGTTAATATCACTGACAGCTTCTGTGTGTGTGTCAGAAAGATTAAGCAGTTGATA	2940
Q	2941	ATGCCAATATGATCAAAAGGAGGCTAGGTTTGTCTATCATCTCAGTTCAAGGCA	3000
D	2941	ATGCCAATATGATCAAAAGGAGGCTAGGTTTGTCTATCATCTCAGTTCAAGGCA	3000
Q	3001	ACGAATCTGSACTCATTTCAATTAACATGACCTTTTACAAAACCCATATGTATAC	3060
D	3001	ACGAATCTGSACTCATTTCAATTAACATGACCTTTTACAAAACCCATATGTATAC	3060
Q	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAATGTAAAGTAAATCTGCTAGAGG	3120
D	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAATGTAAAGTAAATCTGCTAGAGG	3120
Q	3121	AAAACTTTGAGGACATTCATGTCACCTGAAGAAATGGAATGGAATGAAACATTCGA	3180
D	3121	AAAACTTTGAGGACATTCATGTCACCTGAAGAAATGGAATGGAATGAAACATTCGA	3180
Q	3181	GTACAGTACGACATTTAGCCGTAAATACATTAGAGAAAATGTTTTAAAGACGACCT	3240
D	3181	GTACAGTACGACATTTAGCCGTAAATACATTAGAGAAAATGTTTTAAAGACGACCT	3240
Q	3241	CNAGCAATATTATAGAGTAGGTTCCAGTAACTAATGAAGTGGGCTCCAGTATTAATGAA	3300
D	3241	CNAGCAATATTATAGAGTAGGTTCCAGTAACTAATGAAGTGGGCTCCAGTATTAATGAA	3300
Q	3301	TAGGTTCCAGTGATGAAAAATTCNAGCAGAACTAGGTAGAAACAGAGGCGCAAAATTGA	3360
D	3301	TAGGTTCCAGTGATGAAAAATTCNAGCAGAACTAGGTAGAAACAGAGGCGCAAAATTGA	3360
Q	3361	ATGCTATGCTTATAGATTAGGGGTTTGGCAACTGAGGTCTATTAACAAAGTCTTCTGGAA	3420
D	3361	ATGCTATGCTTATAGATTAGGGGTTTGGCAACTGAGGTCTATTAACAAAGTCTTCTGGAA	3420
Q	3421	GTAATTTGAGACATCTGCAAAATTAAGAAATATGAAAGTATGAGTCTGAGCTGTTA	3480
D	3421	GTAATTTGAGACATCTGCAAAATTAAGAAATATGAAAGTATGAGTCTGAGCTGTTA	3480
Q	3481	ATACAGATTTCTCTCATATCTGATTTAGATAACTTAGAAACAGCTTATGGAAGTATGTC	3540
D	3481	ATACAGATTTCTCTCATATCTGATTTAGATAACTTAGAAACAGCTTATGGAAGTATGTC	3540
Q	3541	ATGATCTCAGGTTTGTCTGAGACACTGATGACCTTTGATGATGTGTAATTAAGG	3600
D	3541	ATGATCTCAGGTTTGTCTGAGACACTGATGACCTTTGATGATGTGTAATTAAGG	3600
D	3541	ATGATCTCAGGTTTGTCTGAGACACTGATGACCTTTGATGATGTGTAATTAAGG	3600
Q	3601	AAGTACTAGTTTTTGTCTGAAAATGACATTAAGAAAATTTCTGCTGTTTTTACAAAACGC	3660
D	3601	AAGTACTAGTTTTTGTCTGAAAATGACATTAAGAAAATTTCTGCTGTTTTTACAAAACGC	3660
Q	3661	TCCGAAAAGGAGCTTTAGCAGAGTCTTAGCCCTTTACCCATACATTTGGCTCAGG	3720
D	3661	TCCGAAAAGGAGCTTTAGCAGAGTCTTAGCCCTTTACCCATACATTTGGCTCAGG	3720
Q	3721	GTTACGGAAGAGGGGCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTAGGATG	3780
D	3721	GTTACGGAAGAGGGGCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTAGGATG	3780
Q	3781	AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTAAGTAAACAATATACCTTCTCAGT	3840
D	3781	AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTAAGTAAACAATATACCTTCTCAGT	3840
Q	3841	CTACTAGGATAGCAGCGTTGCTAACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT	3900
D	3841	CTACTAGGATAGCAGCGTTGCTAACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT	3900
Q	3901	TATCATTTGAAGAAATAGCTTAAATGACGTCAGTAAACAGATTAATTTGGCAAGGCACTC	3960
D	3901	TATCATTTGAAGAAATAGCTTAAATGACGTCAGTAAACAGATTAATTTGGCAAGGCACTC	3960
Q	3961	AGGAAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTTCTTCAAGTCA	4020
D	3961	AGGAAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTTCTTCAAGTCA	4020
Q	4021	GTGAATTTGAAGACTTGACTGCAATATCAAAACCCAGATCTCTTCTTGATTTGTTCTT	4080
D	4021	GTGAATTTGAAGACTTGACTGCAATATCAAAACCCAGATCTCTTCTTGATTTGTTCTT	4080
Q	4081	CCAAACAAATGAGGACATCACTGCAAGCCAGGAGTGTCTGATGACAAAGAAATTTG	4140
D	4081	CCAAACAAATGAGGACATCACTGCAAGCCAGGAGTGTCTGATGACAAAGAAATTTG	4140
Q	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTGAAGAAAATATCAAGAAACCAAGCA	4200
D	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTGAAGAAAATATCAAGAAACCAAGCA	4200
Q	4201	TGGAATTTCAAACTTAGGTGAAGACGACTGTGGGTGTGAGAGTGAACAAAGGCTCTGAAG	4260
D	4201	TGGAATTTCAAACTTAGGTGAAGACGACTGTGGGTGTGAGAGTGAACAAAGGCTCTGAAG	4260
Q	4261	ACTGCTCAGGGCTATCTCTCAAGTGAACATTTTAAACACTCGACAGAGGATTAACATG	4320
D	4261	ACTGCTCAGGGCTATCTCTCAAGTGAACATTTTAAACACTCGACAGAGGATTAACATG	4320
Q	4321	AACATTAACCTGATTAAGCTCCAGCAGAAAATGCTGAACATGAAGCTGTGTTGAACAGC	4380
D	4321	AACATTAACCTGATTAAGCTCCAGCAGAAAATGCTGAACATGAAGCTGTGTTGAACAGC	4380
Q	4381	ATGGAGGACGACCTTTTAAACAGTACCTTTCAATCATTAAGTGACTTTCTGCCCTTGAG	4440


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QY 2881 AGACAGTTAATCACTGAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2940
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RESULT 9
AR004673 5914 bp DNA linear PAT 04-DEC-1998
LOCUS AR004673
DEFINITION Sequence 1 from patent US 5747282.
ACCESSION AR004673
VERSION AR004673.1 GI:3965552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5914)
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Hairston,K.D., Shattuck-Bidens,D.M., Tavilgian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
TITLE 17Q-linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5747282-A 1 05-MAY-1998;
FEATURES
source 1..5914
BASE COUNT 2006 a 1156 c 1316 g 1436 t
ORIGIN
Query Match 100.0%; Score 5709.4; DB 6; Length 5914;
Best Local Similarity 100.0%; Pred. No.0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy	5581	TCCATGCAATTGGGGAGATGTGTGTGAAGCACCTGTGTGTACCCGAGAGTGGGTGTGACA	5640
Dd	5581	TCATATGCAATTGGGGAGATGTGTGTGAAGCACCTGTGTGTACCCGAGAGTGGGTGTGACA	5640
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Dd	5641	GTTGTAGCACTTACCAAGTGCACGAGAGCTGACACCTACTGATACCCCAGATGCCCCACA	5700
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RESULT 10

LOCUS	5914 bp	DNA	linear	PAT 04-DEC-1998
DEFINITION	Sequence 1 from patent US 5753441.			
ACCESSION	AR008159			
VERSION	AR008159.1	GI:3967268		

SOURCE Unknown.

Unclassified.

AUTHORS

TITLE	JOURNAL	FEATURES
170-linked breast and ovarian cancer susceptibility gene	Patent: US 5753441-A 1 19-MAY-1998;	Location/Qualifiers

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BASE COUNT	2006 a	1156 c 1316 g 1436 t
ORIGIN		

Query Match	100.0%	Score 5709.4	DB 6	Length 5914
Best Local Similarity	100.0%	Pred. No. 0		
Matches 5710; Conservative	0	Mismatches	1	Indels 0; Gaps 0

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42
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Db 781 CAAAAGGCTGCTTGTGAATTTCTGAGACGGATGTAACAAATACTGAACATCATCAAC 840

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Db 1081 GGGCTGGAGTAAGGAAA CATGTAATGATAGGCGACTCCGACACAGAAAAAAGGTAG 1140

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Qy	1441	TATGTAAAGTGAAGAGTCTACTCCCAATCAGTAGAGTATATATTGAAGCAAAATAT	1500
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LOCUS AR136942 5914 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6162897.
ACCESSION AR136942
VERSION AR136942.1 GI:14478192
KEYWORDS
SOURCE unknown.

ORGANISM Unknown.
 Unclassified.
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 REFERENCE Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
 AUTHORS Harshman, K.D., Shattuck-Eidens, D.M., Tavtiglian, S.V., Wiseman, R.W.
 TITLE 17q-linked breast and ovarian cancer susceptibility gene
 JOURNAL Patent: US 6162897-A 1 19-DEC-2000;
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QY	2641	GGGAAACAGACATAGAAATGAGAAAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
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QY	2701	TCAAGTTTCAAGAGGCGCACTGATTTGCTCTGTTTTCAAATCCAGAAATCCAGAAAGG	2760
Db	2701	TCAAGTTTCAAGAGGCGCACTGATTTGCTCTGTTTTCAAATCCAGAAATCCAGAAAGG	2760
QY	2761	AATGTGCAAACTTCTCTGCGCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGAGCTT	2820
Db	2761	AATGTGCAAACTTCTCTGCGCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGAGCTT	2820
QY	2821	TTGAATGTGAACAAAAGAGAAAGAAATCAAGAAAGATAGTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGAGAAAGAAATCAAGAAAGATAGTCTTAATATCAAGCTGTAC	2880
QY	2881	AGACAGTTTAATTCACCTGAGGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881	AGACAGTTTAATTCACCTGAGGCTTTCCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA	2940
QY	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTTTGTCTATCATCTCAGTTCAAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTTTGTCTATCATCTCAGTTCAAGGCA	3000
QY	3001	ACGAACCTGCACTTACTCTCCAAATTAACATGACCTTTTACAAAAACCATATGCTATAC	3060

Dp	3001	ACGAAACTGAGCTCAATTACTCCAAATAAACATGAGCTTTTACAAACCCCATATGCTATAC	3060
Qy	3061	CACCACTTTTCCCATCAAGTCATTTGTTTAAACCTAATGTAAAGAAAATCTGCTAAGG	3120
Dp	3061	CACCACTTTTCCCATCAAGTCATTTGTTTAAACCTAATGTAAAGAAAATCTGCTAAGG	3120
Qy	3121	AAAACTTTAGAGAACATTCAATGTCACTGTAAGAGAAATGGGAAATGAGAACCTTCCA	3180
Dp	3121	AAAACTTTAGAGAACATTCAATGTCACTGTAAGAGAAATGGGAAATGAGAACCTTCCA	3180
Qy	3181	GTACGTAGAGACAATTAGCGGCTAATACATTAAGAGAAAATGTTTAAAGAACCCAGCT	3240
Dp	3181	GTACGTAGAGACAATTAGCGGCTAATACATTAAGAGAAAATGTTTAAAGAACCCAGCT	3240
Qy	3241	CAAGCAATATTAAATGAAGTAGGTTCCAGTACTAAATGAAGTGGGCTCCAGTATTAATGAA	3300
Dp	3241	CAAGCAATATTAAATGAAGTAGGTTCCAGTACTAAATGAAGTGGGCTCCAGTATTAATGAA	3300
Qy	3301	TAGGTTCCAGTATGAAAAACATTCAAGCAGAACTAGAGTAAACAGAGGGCCAAATTTGA	3360
Dp	3301	TAGGTTCCAGTATGAAAAACATTCAAGCAGAACTAGAGTAAACAGAGGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAAGTATGAGGGGTTTTGCAACCTGAGGCTATTAACCAAGTCTTCTGGAA	3420
Dp	3361	ATGCTATGCTTAAGTATGAGGGGTTTTGCAACCTGAGGCTATTAACCAAGTCTTCTGGAA	3420
Qy	3421	GTAATTTGTAACATCTGTAATAAATAAAGCAAGAAATGAAGAAATGTTTCAACTGTTA	3480
Dp	3421	GTAATTTGTAACATCTGTAATAAATAAAGCAAGAAATGAAGAAATGTTTCAACTGTTA	3480
Qy	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTAGAACACGCTTATGGGAAATGTC	3540
Dp	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTAGAACACGCTTATGGGAAATGTC	3540
Qy	3541	ATGCATCTCAGGTTGTTCTCTGAGACACCTGATGACCTGTATGATGATGGTAAATTAAGG	3600
Dp	3541	ATGCATCTCAGGTTGTTCTCTGAGACACCTGATGACCTGTATGATGATGGTAAATTAAGG	3600
Qy	3601	AAGATACTAGTTTGTGCTGAAAAATACATTAAGAGAAATGTTCTGCTGTTTTAGCAAAAGC	3660
Dp	3601	AAGATACTAGTTTGTGCTGAAAAATACATTAAGAGAAATGTTCTGCTGTTTTAGCAAAAGC	3660
Qy	3661	TCCAGAAAGAGAGAGCTTAGCAGAGTCCCTTTCACCCATACACATTTGGCTCAGG	3720
Dp	3661	TCCAGAAAGAGAGAGCTTAGCAGAGTCCCTTTCACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTACCGAAGAGGGGCCAAGAAATTAAGTCCCTAGAGAGAACTTTATCTAGTAGAGTG	3780
Dp	3721	GTTACCGAAGAGGGGCCAAGAAATTAAGTCCCTAGAGAGAACTTTATCTAGTAGAGTG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCACACTTGTGTAATTTGGTAAAGTAAACATAATACCTTCTCAGT	3840
Dp	3781	AAGAGCTTCCCTGCTTCCACACTTGTGTAATTTGGTAAAGTAAACATAATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCGGTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Dp	3841	CTACTAGGCATAGCACCGGTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCTTTGAAGAAATAGCTTAAATGATGACGTAAACAGGTAAATTTGGCAAAAGGCATCTC	3960
Dp	3901	TATCTTTGAAGAAATAGCTTAAATGATGACGTAAACAGGTAAATTTGGCAAAAGGCATCTC	3960
Qy	3961	AGGAACATCACCTTAGTAGAGAAACAAATATTTCTGAGCTTGTGTTTCTTCCACAGTGCA	4020
Dp	3961	AGGAACATCACCTTAGTAGAGAAACAAATATTTCTGAGCTTGTGTTTCTTCCACAGTGCA	4020
Qy	4021	GTGAATTTGAAGACTTGACTTGCAAAATACAAACCCAGAGATCTTCTTGAATTTGGTCTT	4080
Dp	4021	GTGAATTTGAAGACTTGACTTGCAAAATACAAACCCAGAGATCTTCTTGAATTTGGTCTT	4080
Qy	4081	CCAAACAAATAGGCAATGATGTTGTAAGACCCAGGAGTTGGTCTGATGCAACGAATTTGG	4140

Db 121 TGAATTAATCTGCTCTTGCCTGGAAGATACAAAATGTCATTAATGCTATGACAGAAA 180
Qy 181 TCTTAAGCTGCCATCTGTCTGAGTTGATCAAGAAACCTGTCCCAAACTGTGACC 240
Db 181 TCTTAAGCTGCCATCTGTCTGAGTTGATCAAGAAACCTGTGTCCCAAACTGTGACC 240
Qy 241 ACATATTTTGGAAATTTTGCATGCTGAAACCTCTCAACAGAGAAAGGCGCTTCAAGT 300
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Qy 301 GTCTTTATGTAAGATATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
Db 301 GTCTTTATGTAAGATATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
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Db 361 AACTTTTGAAGCTATTTGAAAATCAATTTGTCTTTTCACTTCAAGATTTTGAAGT 420
Qy 421 ATGCAACAGCTATATTTTGCAGAAAAGAAATTAATCTCTGAAACATCTTAAAGATG 480
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Db 541 AACCAGAAATCCCTTCTTGAAGAAACAGCTCAGTGTCACTCTTCACTTGAAG 600
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Db 601 CTGTGAGAACTCTGAGAGCAAAAGCAGCGATACAACTCAAAAAGAGCTGTCTCAATG 660
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Qy 901 ATCAGGGATTTCTGTTCAAACTGACATGTGAGCGCATGTGGCAAAATACATGCGCA 960
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REFERENCE 1 (bases 1 to 5914)
AUTHORS Shattuck-Bidens, D.M., Simard, J., Durocher, F., Emi, M. and Nakamura, Y.
TITLE Linked breast and ovarian cancer susceptibility gene
JOURNAL Patent: US 5709999-A 1 20-JAN-1998;
FEATURES
source location/qualifiers
1..5914 /organism="unknown"
BASE COUNT 2006 a 1156 c 1316 g 1436 t
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTCTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATACTGGCC 60
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Db 121 TGAATTTATCTGCTCTGCGGTTGAGAGATGACAAATGTCATTAATGCTATGAGAAA 180
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QY 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCTGCAATCTTAAGATG 480
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QY 481 AAGTTTCATCATCAAGATGAGGCTACAGAAACGTGCAAAAGACTTCTACAGAGT 540
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D 2101 GGCACAGCAGAAACCTCAACTCATGAGAGTTAAAGAACTTGCAACCTGAGGCAAGAGA 2160
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QY	2821	TTGAATGTGAACAAAGAGAGAGAAATCAAGGAAAGAAAGAGCTATATTCAGGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAGAGAGAAATCAAGGAAAGAAAGAGCTATATTCAGGCTGTAC	2880
QY	2881	AGACGTTAATATCATCTGAGGCTTTCTGTGCTTGGTCAGAAAGATTAAGCAGTTGATA	2940
Db	2881	AGACGTTAATATCATCTGAGGCTTTCTGTGCTTGGTCAGAAAGATTAAGCAGTTGATA	2940
QY	2941	ATGCGCAATGTATGTCAAGAGGCTTAGGTTTTGTCTATCATCTGATTCAGAGCA	3000
Db	2941	ATGCGCAATGTATGTCAAGAGGCTTAGGTTTTGTCTATCATCTGATTCAGAGCA	3000
QY	3001	ACGAAATCGAGCTCATTTACTCCAAATTAACATGAGCTTTTTCACAAACCCATATGCTATAC	3060
Db	3001	ACGAAATCGAGCTCATTTACTCCAAATTAACATGAGCTTTTTCACAAACCCATATGCTATAC	3060
QY	3061	CACCACTTTTTCCCATCAAGTCATTTGTTTAAACTAAATGTAGAAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTTCCCATCAAGTCATTTGTTTAAACTAAATGTAGAAAATCTGCTAGAGG	3120
QY	3121	AAAACCTTGAGGAACATTCATATGTCACCTGAAAGAAATGGGAAATGAGAACATTCAC	3180
Db	3121	AAAACCTTGAGGAACATTCATATGTCACCTGAAAGAAATGGGAAATGAGAACATTCAC	3180
QY	3181	GTACAGTGAGCACAATTAGCCGTATTAACATTAGAGAAATGTTTTTAAAGAGCAGCT	3240
Db	3181	GTACAGTGAGCACAATTAGCCGTATTAACATTAGAGAAATGTTTTTAAAGAGCAGCT	3240
QY	3241	CAAGCAATATTATGAGTAGGTTCCAGTACTAATGAAAGTGGGCTCCAGTATTAATGAA	3300
Db	3241	CAAGCAATATTATGAGTAGGTTCCAGTACTAATGAAAGTGGGCTCCAGTATTAATGAA	3300
QY	3301	TAGGTTCCAGTATGAAAAACATTCAAGAGAACTGAGTAGAAACGAGGGCCAAATTTGA	3360
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QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTTATTAACAAAGTCTTCTCGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTTATTAACAAAGTCTTCTCGGAA	3420
QY	3421	GTAATTGTAGCATCTCTGAAAAATGAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATTGTAGCATCTCTGAAAAATGAAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA	3480
QY	3481	ATACAGATTTTCTCTCATATCTGATTTTCAAGATTACTTGAAACAGCTTATGGGAAGTATC	3540
Db	3481	ATACAGATTTTCTCTCATATCTGATTTTCAAGATTACTTGAAACAGCTTATGGGAAGTATC	3540
QY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATATGTAATTAAGG	3600
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QY	3601	AAGATACTAGTTTGTGCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTTGAACAAACG	3660
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QY	3661	TCCAGAAAGAGAGCTTAGCAGAGGCTCTAGCCCTTTTACCCCATACAAATTTGGCTCAGG	3720
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QY	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCCCTGAAAGAGAACTTATCTAGTGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCCCTGAAAGAGAACTTATCTAGTGAGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGGTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900

Db	3841	CTACTAGGCAATGACACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTAT	3900
Qy	3901	TATCATGGAAGATAGCTTTAAATGACCTGACATAACAGTAAATATGCGCAAGGCAATCTC	3960
Db	3901	TATCATGGAAGATAGCTTTAAATGACCTGACATAACAGTAAATATGCGCAAGGCAATCTC	3960
Qy	3961	AGGAACATACACCTTAGTGAAGAAACAAATGTTGCTAGCTGCTTTCTTCAAGTGA	4020
Db	3961	AGGAACATACACCTTAGTGAAGAAACAAATGTTGCTAGCTGCTTTCTTCAAGTGA	4020
Qy	4021	GTGAATTGGAAGACTTGACTCAATATCAACACCCAGATCCCTTTCTTGATTGGTCTT	4080
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Qy	4081	CCAAACAAATGAGGCATCAGTCTGAAAACCGAGGAGTTGGTCTGAGTGACAGGAATTGG	4140
Db	4081	CCAAACAAATGAGGCATCAGTCTGAAAACCGAGGAGTTGGTCTGAGTGACAGGAATTGG	4140
Qy	4141	TTTTCAGATGATGAAAGAAAGAGAAACGGGCTTTGAAAGAAAATATACAAAGAAAGAAACA	4200
Db	4141	TTTTCAGATGATGAAAGAAAGAGAAACGGGCTTTGAAAGAAAATATACAAAGAAAGAAACA	4200
Qy	4201	TGGAATTCAACTTAGTGAAGACACATCTGGGGTGTGAGAGTGAACAACAGCCTCTGTAG	4260
Db	4201	TGGAATTCAACTTAGTGAAGACACATCTGGGGTGTGAGAGTGAACAACAGCCTCTGTAG	4260
Qy	4261	ACTGCTCAGGGCTATCCCTCAGAGTGCATTTTAAACCACTCAGCAGAGGGATACCATGC	4320
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Db	4441	ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGAGATTAACTTTCACAGAAAAATA	4500
Qy	4501	GTGAATACCTTATTAAGCCAGATATCAGAGGCCCTTTCTGCTGACAAAGTTTGAAGTGTG	4560
Db	4501	GTGAATACCTTATTAAGCCAGATATCAGAGGCCCTTTCTGCTGACAAAGTTTGAAGTGTG	4560
Qy	4561	CAGATAGTTCACAGTAAATAATTAAGAACAGAGATGGAAGGTCAATCCCTCTTAAT	4620
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AR048660					
LOCUS	AR048660	5711 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 4 from patent US 5823328.				

VERSION	AR048660.1	GI:5971003
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	

REFERENCE	1 (bases 1 to 5711)
AUTHORS	King,M.-C., Friedman, L., Ostermeyer,B., Rowell,S., Lynch,E., Szabo,C. and Lee,M.
TITLE	Genetic markers for breast, ovarian, and prostatic cancer
JOURNAL	Patent: US 5821328-A 4 13-OCT-1998;
FEATURES	Location/Qualifiers

	source	1..5711
BASE COUNT	/organism="unknown"	
ORIGIN	1956 a 1099 c 1275 g 1381 t	

Query Match	99.9%	Score 5707.8	DB 6	Length 5711
Best Local Similarity	100.0%	Pred. No. 0		
Matches 5709; Conservative	0	Mismatches 2	Indels 0	Gaps 0

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2007-08-09 10:10:10

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Db 5701 GGCACACTGGA 5711

Mon Jun 16 08:11:53 2003

Search completed: June 13, 2003, 08:24:59
Job time : 14055 secs

us-09-734-672-3.rge

Page 45

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:07:45 ; Search time 1106 Seconds
(without alignments)
11628.537 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711

Sequence: 1 AGCTCCGCTGAGACTCTCTG.....TCCCCACAGCACTACTGTA 5711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	19	AAV46449
2	5711	100.0	5711	21	AAV46449
3	5711	100.0	5711	17	AAV46449
4	5710.6	100.0	5711	19	AAV46449
5	5710.6	100.0	5711	19	AAV46449
6	5710.6	100.0	5711	19	AAV46449
7	5710.6	100.0	5711	19	AAV46449
8	5710.6	100.0	5711	19	AAV46449
9	5710.6	100.0	5711	19	AAV46449

10	5710.6	100.0	5711	19	AAV46449	Human BRCA1 omi2 p
11	5709.4	100.0	5712	18	AAV46449	Human breast and o
12	5709.4	100.0	5712	21	AAV46449	BRCA1 gene sequenc
13	5709.4	100.0	5714	17	AAV46449	BRCA1, breast and
14	5709.4	100.0	5714	17	AAV46449	BRCA1 coding sequ
15	5709.4	100.0	5714	17	AAV46449	BRCA1, breast and
16	5707.8	99.9	5711	17	AAV46449	BRCA1 allele #8403
17	5707.8	99.9	5711	17	AAV46449	BRCA1 allele #7408
18	5707.8	99.9	5711	18	AAV46449	Mutant BRCA1 allel
19	5707.8	99.9	5711	18	AAV46449	Mutant BRCA1 allel
20	5707.8	99.9	5711	19	AAV46449	Tumorigenic BRCA1
21	5707.8	99.9	5711	19	AAV46449	Tumorigenic BRCA1
22	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
23	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
24	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
25	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
26	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
27	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
28	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
29	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
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44	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi
45	5707.8	99.9	5714	17	AAV46449	Mutated BRCA1 codi

ALIGNMENTS

RESULT 1	AAV46449	standard; cDNA; 5711 BP.
ID	AAV46449;	
AC	AAV46449;	
XX		
DT	18-NOV-1998	(first entry)
XX		
DE	Human BRCA1 omi2 cDNA.	
XX		
KW	BRCA1; omi2; human; breast and ovarian cancer predisposing gene;	
KW	polymorphism; susceptibility; anti-oncogene; tumour suppressor;	
KW	chromosome 17q; ss.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	120..5711
FT		/tag= a
XX		/product= "BRCA1 omi2 protein"
XX		
PN	US5750400-A.	
XX		
PD	12-MAY-1998.	
XX		
PF	12-FEB-1997;	97US-0798691.
XX		
PR	12-FEB-1996;	96US-0598591.
XX		
PR	12-FEB-1997;	97US-0798691.
XX		
PA	(ONCO-) ONCORMED INC.	
XX		

PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI Schelker DB, Zeng B;
DR WPI; 1998-296774/26.
DR P-PSDB; AAM76099.
PT BRCA1 omi gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
PS Claim 2d; Column 41-46; 54dp; English.
XX
CC This sequence encodes the human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi2 gene. This sequence and polymorphic variations of
CC this sequence are useful for the identification of an individual who may
CC or may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome 17q
CC which is known to be linked to cancer susceptibility, especially breast
CC cancer. Cells containing a mutation in this gene lose the wild-type
CC function of BRCA1 and are more susceptible to cancers.
XX
SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1383 T; 0 other;
Query Match 100.0%; Score 5711; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 2701 TCAAGGTTTCAAGGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2760
 QY 2761 AATGTGCAACATTTCTGCGCACTTGGGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
 DB 2761 AATGTGCAACATTTCTGCGCACTTGGGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
 QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880

DB 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880
 QY 2881 AGACATTAATATCACTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 DB 2881 AGACATTAATATCACTGACAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
 QY 2941 ATGCCAAATGTAGTATCAAGAGGCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000
 DB 2941 ATGCCAAATGTAGTATCAAGAGGCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000
 QY 3001 ACAGAACTGAGTCACTTATCTCCAAATTAACATGAGCTTTTACAAACCAATATCTATAC 3060
 DB 3001 ACAGAACTGAGTCACTTATCTCCAAATTAACATGAGCTTTTACAAACCAATATCTATAC 3060
 QY 3061 CACCACTTTTCCCACTCAAGTCACTTTGTTTAACTAATGTAAGAAAAATCTGCTAGAG 3120
 DB 3061 CACCACTTTTCCCACTCAAGTCACTTTGTTTAACTAATGTAAGAAAAATCTGCTAGAG 3120
 QY 3121 AAAAATTTGAGGAAACATTCATGCTCACTGAAAGAGAAATGGGAATGAGAACATTCGAA 3180
 DB 3121 AAAAATTTGAGGAAACATTCATGCTCACTGAAAGAGAAATGGGAATGAGAACATTCGAA 3180
 QY 3181 GTACAGTGAACAATTAACCTGATTAATGAGAAATGTTTAAAGAACCAAGCT 3240
 DB 3181 GTACAGTGAACAATTAACCTGATTAATGAGAAATGTTTAAAGAACCAAGCT 3240
 QY 3241 CAAGCAATTTAATGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGAAG 3300
 DB 3241 CAAGCAATTTAATGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGAAG 3300
 QY 3301 TAGGTTCCAGTGAATGAAGAACTTCAAGCAAGAACTAGTGAAGAAACAGAGGCCCCAAAT 3360
 DB 3301 TAGGTTCCAGTGAATGAAGAACTTCAAGCAAGAACTAGTGAAGAAACAGAGGCCCCAAAT 3360
 QY 3361 ATGCTATGCTTGAAGTGAAGGTTTTCGAACTGAGGCTATTAACCAAGTCTTCTGGA 3420
 DB 3361 ATGCTATGCTTGAAGTGAAGGTTTTCGAACTGAGGCTATTAACCAAGTCTTCTGGA 3420
 QY 3421 GTTATGTAAGCATCTGTAATTAAGAAACCAAGAAATGAAGAGTTCAGACTGTA 3480
 DB 3421 GTTATGTAAGCATCTGTAATTAAGAAACCAAGAAATGAAGAGTTCAGACTGTA 3480
 QY 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAACCTTAAAGCAAGCTTAATGGAAGT 3540
 DB 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAACCTTAAAGCAAGCTTAATGGAAGT 3540
 QY 3541 ATGCAATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAAGATGAGTGAAGTAAAG 3600
 DB 3541 ATGCAATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAAGATGAGTGAAGTAAAG 3600
 QY 3601 AAGATCTCTGTTTGTCTGAAATGACATTAAGAAAGTCTGCTGTTTAAAGAAAGG 3660
 DB 3601 AAGATCTCTGTTTGTCTGAAATGACATTAAGAAAGTCTGCTGTTTAAAGAAAGG 3660
 QY 3661 TCCAGAAAGAGAGCTTACAGAGGCTTACAGGCTTTCACCAATACACTTGGGCTCAG 3720
 DB 3661 TCCAGAAAGAGAGCTTACAGAGGCTTTCACCAATACACTTGGGCTCAG 3720
 QY 3721 GTTACCGAAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGT 3780
 DB 3721 GTTACCGAAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAGT 3780
 QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAGTAAACATATATCTTCTCAGT 3840
 DB 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAGTAAACATATATCTTCTCAGT 3840
 QY 3841 CTACTAGGATGACACCGTTCCTACAGAGTGTCTGTAAAGAACACAGAGGAAATTTAT 3900
 DB 3841 CTACTAGGATGACACCGTTCCTACAGAGTGTCTGTAAAGAACACAGAGGAAATTTAT 3900
 QY 3901 TATCATGTAAGATAGCTTAAATGAATGAGTCACTGAGTAAATGTTGCAAGGCACTCTC 3960

PR 12-DEC-1997; 97US-0798691.
 XX (GENE-) GENE LOGIC INC.
 XX
 PI Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD,
 PI Ciliz BS;
 XX
 DR WPI; 2000-646756/62.
 DR P-PSDB; AAB24219.
 XX
 PT New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful
 PT in gene therapy, especially for preventing or treating breast or
 PT ovarian cancer, as well as for diagnosing or monitoring breast or
 PT ovarian cancer -
 XX
 XX
 PS Example 4; Column 59-66; 56pp; English.
 CC AAC60793 to AAC60795 encode the human BRCA1 (om1-3) proteins given in
 CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17
 CC mapping to position 17q21. The BRCA1 (om12) coding sequence is
 CC specifically claimed in the present invention. The BRCA1 (om12) coding
 CC sequence is useful in gene therapy, especially for preventing or treating
 CC breast or ovarian cancer. It is also useful for diagnosing or monitoring
 CC breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence
 CC is useful for: (a) identifying individuals having BRCA1 gene mutations
 CC and having an increased genetic susceptibility to breast or ovarian
 CC cancer, or identifying a mutation that increases the genetic
 CC susceptibility to breast or ovarian cancer; (b) avoiding
 CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)
 CC determining the presence of a previously unknown mutation in the BRCA1
 CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine
 CC the presence of either polymorphic alleles or mutations; and (e)
 CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA
 CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,
 CC which are used in an example from the present invention.
 CC
 XX
 SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1383 T; 0 other;
 Query Match 100.0%; Score 5711; DB 21; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 AAGTTCTATCATCCAAAGATGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGT 540
 |||||
 DB 481 AAGTTCTATCATCCAAAGATGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGT 540
 QY 541 AACCCGAAAATCCTTCTCAGAGAAACAGTCTCAGTGTCCAACTCTCTAACCTTGAA 600
 |||||
 DB 541 AACCCGAAAATCCTTCTCAGAGAAACAGTCTCAGTGTCCAACTCTCTAACCTTGAA 600
 QY 601 CTGTGAAACTCTGAGACAAAGACCGGATACACCTCAAAAAGAGTCTGTCTAACAT 660
 |||||
 DB 601 CTGTGAAACTCTGAGACAAAGACCGGATACACCTCAAAAAGAGTCTGTCTAACAT 660
 QY 661 AATTGGATCTGATCTTCTGAAAGATACCGTTAATAAGCACTTAATGAGTGGAG 720
 |||||
 DB 661 AATTGGATCTGATCTTCTGAAAGATACCGTTAATAAGCACTTAATGAGTGGAG 720
 QY 721 ATCAAGAAATGTTACAAATCACCCCTCAAGAAACAGGATGAATCAGTTTGGATCT 780
 |||||
 DB 721 ATCAAGAAATGTTACAAATCACCCCTCAAGAAACAGGATGAATCAGTTTGGATCT 780
 QY 781 CAAAAAAGCTGCTGTGAAATTTTCTGAGACGATGTAACAATCTGAAACATCATCAC 840
 |||||
 DB 781 CAAAAAAGCTGCTGTGAAATTTTCTGAGACGATGTAACAATCTGAAACATCATCAC 840
 QY 841 CCAGTAATATGATTTGAAACACCACTGAGAAAGGCTGAGAGCATCCAGAAAGT 900
 |||||
 DB 841 CCAGTAATATGATTTGAAACACCACTGAGAAAGGCTGAGAGCATCCAGAAAGT 900
 QY 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGATGAGGATGAGCAAAATCTCATGCCA 960
 |||||
 DB 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGATGAGGATGAGCAAAATCTCATGCCA 960
 QY 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTACTTAAGACAGATGATGAGAA 1020
 |||||
 DB 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTACTTAAGACAGATGATGAGAA 1020
 QY 1021 AGGCTGAATTCGTATTAAGCAACAGCTGGCTTACAGAGGACCAATCAAGAT 1080
 |||||
 DB 1021 AGGCTGAATTCGTATTAAGCAACAGCTGGCTTACAGAGGACCAATCAAGAT 1080
 QY 1081 GGGCTGGAAGTAAGAAACATGATGATGATGAGCGGACTCCAGACAGAAAAAAGTGA 1140
 |||||
 DB 1081 GGGCTGGAAGTAAGAAACATGATGATGATGAGCGGACTCCAGACAGAAAAAAGTGA 1140
 QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGATGAATGAAGCAGAAACTGCTATGCT 1200
 |||||
 DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGATGAATGAAGCAGAAACTGCTATGCT 1200
 QY 1201 CAGAGAACTCTGAGATGATGAGAAATGTTCTGATTAACATTAATACAGATTCAGA 1260
 |||||
 DB 1201 CAGAGAACTCTGAGATGATGAGAAATGTTCTGATTAACATTAATACAGATTCAGA 1260
 QY 1261 AAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 |||||
 DB 1261 AAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
 QY 1321 GGGAGTCTGAATCAAAATGCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380
 |||||
 DB 1321 GGGAGTCTGAATCAAAATGCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380
 QY 1381 AATATTCGCTCTTCAAGAAATAGACTTCTGAGCAATGATCTCTAATGAGGCTTTAA 1440
 |||||
 DB 1381 AATATTCGCTCTTCAAGAAATAGACTTCTGAGCAATGATCTCTAATGAGGCTTTAA 1440
 QY 1441 TATGTAAGTGAAGAGTTCATCCAAATCAGTGAAGATATATGGAAGCAAAATAT 1500
 |||||
 DB 1441 TATGTAAGTGAAGAGTTCATCCAAATCAGTGAAGATATATGGAAGCAAAATAT 1500
 QY 1501 TTGGGAAAACCTATGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
 |||||
 DB 1501 TTGGGAAAACCTATGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560

QY	1561	TAATTAATGAGACATTTGTTACTGAGCCACAGATATATCAAGAGCTGCCCTCCACAAATA	1620
Dp	1561	TAATTAATGAGAGCATTTGTTACTGAGCCACAGATATATCAAGAGAGCTGCCCTCCACAAATA	1620
QY	1691	AAATTAACCGTAAAGAGAGACCTACATCAGGCGTTCACTCGAGGATTTTATCAAGAAAG	1680
Dp	1621	AAATTAACCGTAAAGAGAGACCTACATCAGGCGTTCACTCGAGGATTTTATCAAGAAAG	1680
QY	1691	CAGATTTTGGCAGGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAACGAGNC	1740
Dp	1691	CAGATTTTGGCAGGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAACGAGNC	1740
QY	1741	AGATGCTCAAGTGTGAATATTAATTAATGCTCATGAGATTAACAAACAGTATTT	1800
Dp	1741	AGAAATGCTCAAGTGTGAATATTAATTAATGCTCATGAGATTAACAAACAGTATTT	1800
QY	1801	CTATTCAAAATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAAGATCTGCTTTCA	1860
Dp	1801	CTATTCAAAATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAAGATCTGCTTTCA	1860
QY	1861	AAACGAAAGCTGAACTTAATTAAGCAGCAGATATTAAGCAATATGGAATCTCGAATTAATAATCC	1920
Dp	1861	AAACGAAAGCTGAACTTAATTAAGCAGCAGATATTAAGCAATATGGAATCTCGAATTAATAATCC	1920
QY	1921	ACAATTTCAAAAGCCTTAATAAAGATAGCGTGAGGAGAAGTCTTCTACAGGCATATTC	1980
Dp	1921	ACAATTTCAAAAGCCTTAATAAAGATAGCGTGAGGAGAAGTCTTCTACAGGCATATTC	1980
QY	1991	ATGCGCTTGAATCTACTAGTCAGTGAATCTTAAGCCCATTAATTTGTAATGCAATTCGAAA	2040
Dp	1991	ATGCGCTTGAATCTACTAGTCAGTGAATCTTAAGCCCATTAATTTGTAATGCAATTCGAAA	2040
QY	2041	TTGATAGTTGTTCTTAAGCAGTGAAGATTAAGAAAAAAGATACCAACCAATATGCGACGTCA	2100
Dp	2041	TTGATAGTTGTTCTTAAGCAGTGAAGATTAAGAAAAAAGATACCAACCAATATGCGACGTCA	2100
QY	2101	GGCAGCAGAGAAACCTTAACACTCATGGAAGTTAAAGAACTTGCAACTGAGCCCAAGAGA	2160
Dp	2101	GGCAGCAGAGAAACCTTAACACTCATGGAAGTTAAAGAACTTGCAACTGAGCCCAAGAGA	2160
QY	2161	GTAACCAACCCAAATGAACAGACAGTAATAACACATGAGAGATCTTTCCACAGCTGA	2220
Dp	2161	GTAACCAACCCAAATGAACAGACAGTAATAACACATGAGAGATCTTTCCACAGCTGA	2220
QY	2221	AGTTAACAAATGACCTGGTCTTTTACTTAAGTGTTCAAATACAGCAGTAACCTTAAGAGAT	2280
Dp	2221	AGTTAACAAATGACCTGGTCTTTTACTTAAGTGTTCAAATACAGCAGTAACCTTAAGAGAT	2280
QY	2281	TTGTCAATCTTAAGCCTTCCAAAGAGAAAAAGAGAGAAATCTAGAAACAGTTAAAGTGT	2340
Dp	2281	TTGTCAATCTTAAGCCTTCCAAAGAGAAAAAGAGAGAAATCTAGAAACAGTTAAAGTGT	2340
QY	2341	CTAATAATGCTGGAAGACCCCAAAAGATCTCATGTTTAAGTGGAGAAAGGTTTTCGAACTG	2400
Dp	2341	CTAATAATGCTGGAAGACCCCAAAAGATCTCATGTTTAAGTGGAGAAAGGTTTTCGAACTG	2400
QY	2401	AAAAGATCTGTAGAGAGTGAAGCAGTATTTTCAATGGTGAACCTGTATGATTAATGGAACCTGAGG	2460
Dp	2401	AAAAGATCTGTAGAGAGTGAAGCAGTATTTTCAATGGTGAACCTGTATGATTAATGGAACCTGAGG	2460
QY	2461	AAAAGATCTGTTACTGGAAGTTAGCACTTAAGGGAAGCAGAAAAACAGAACCAATTAAT	2520
Dp	2461	AAAAGATCTGTTACTGGAAGTTAGCACTTAAGGGAAGCAGAAAAACAGAACCAATTAAT	2520
QY	2521	GTTGTAGTCAAGTGTGACGATTTGAAAAACCCCAAGGGAATTAATTCATGTTGTTCGAAAG	2580
Dp	2521	GTTGTAGTCAAGTGTGACGATTTGAAAAACCCCAAGGGAATTAATTCATGTTGTTCGAAAG	2580
QY	2581	ATAATAGAAATGACACAGAGGCTTAATGATTCATTTGGGACATGAAATTAACACAGCTC	2640
Dp	2581	ATAATAGAAATGACACAGAGGCTTAATGATTCATTTGGGACATGAAATTAACACAGCTC	2640
QY	2641	GGGAAACAGCATAGAAATGGAAGAAATGAAATCTGATGCTCAGTATTTGCAGAAATTCAT	2700

Db	2641	GGGAAACAAACATGAAATGGAAGGAAAGTGAACCTTGATGCTCAGTATTTGCAATATCAAT	2700
Oy	2701	TCAAGGTTTCAAAAGCCCAAGTCATTTGCTCTGTTTTCAAATCCAGAAATGCAAGAGG	2760
Db	2701	TCAAGGTTTCAAAAGCCCAAGTCATTTGCTCTGTTTTCAAATCCAGAAATGCAAGAGG	2760
Oy	2761	AATGTCACATCTCTCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCATT	2820
Db	2761	AATGTCACATCTCTCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Oy	2821	TTGAAATGTGAACAAAAGGAAGAAATCAAGSAAAGATGAGCTTAATCAAGCTGTAC	2880
Db	2821	TTGAAATGTGAACAAAAGGAAGAAATCAAGSAAAGATGAGCTTAATCAAGCTGTAC	2880
Oy	2881	AGACAGTTAATATCACTGAGAGGCTTTCCTGTTGTGTCAGAAAGATPAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGAGAGGCTTTCCTGTTGTGTCAGAAAGATPAGCCAGTTGATA	2940
Oy	2941	ATGCGAAATGATATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA	3000
Db	2941	ATGCGAAATGATATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGCA	3000
Oy	3001	ACGAAACTGACATCTTACCTCCAAATAAACATGAGCTTTTCAAAACCCATATGATAC	3060
Db	3001	ACGAAACTGACATCTTACCTCCAAATAAACATGAGCTTTTCAAAACCCATATGATAC	3060
Oy	3061	CACACATTTTCCCATCAAGTCATTTGTTTAAACATAAATGTAAGAAATATGCTTAAGG	3120
Db	3061	CACACATTTTCCCATCAAGTCATTTGTTTAAACATAAATGTAAGAAATATGCTTAAGG	3120
Oy	3121	AAAACTTTGAGGAACATTCATGTCCACTGAAAGGAATGGGAATGAGAACATTCGAA	3180
Db	3121	AAAACTTTGAGGAACATTCATGTCCACTGAAAGGAATGGGAATGAGAACATTCGAA	3180
Oy	3181	GTACAGTGAACCAATTAAGCCGTAATTAATTAGAGAAATGTTTTTAAAGAACCCAGCT	3240
Db	3181	GTACAGTGAACCAATTAAGCCGTAATTAATTAGAGAAATGTTTTTAAAGAACCCAGCT	3240
Oy	3241	CAAGCAATTTAATGAAAGTAGTCCAGACTAAATGAAGTGGGCTCCAGTATTAATGAA	3300
Db	3241	CAAGCAATTTAATGAAAGTAGTCCAGACTAAATGAAGTGGGCTCCAGTATTAATGAA	3300
Oy	3301	TAGGTTCCAGTGTGAAAAATTCAAGCAGAACTAGTAGAGAAACAGAGGCCAAATATGA	3360
Db	3301	TAGGTTCCAGTGTGAAAAATTCAAGCAGAACTAGTAGAGAAACAGAGGCCAAATATGA	3360
Oy	3361	ATGCTATGCTTAAGTTAGGGGTTTGGCACTGAGAGCTTAATTAACAAGTCTTCTGGAA	3420
Db	3361	ATGCTATGCTTAAGTTAGGGGTTTGGCACTGAGAGCTTAATTAACAAGTCTTCTGGAA	3420
Oy	3421	GTAAATGTAGCAATCCGGAATTAATAAACAAGATTAAGAAGTAGTTCAGACTGTA	3480
Db	3421	GTAAATGTAGCAATCCGGAATTAATAAACAAGATTAAGAAGTAGTTCAGACTGTA	3480
Oy	3481	ATAAGATTTCTCTCCATATCTGATTTTCAGATTAAGAAACAGCTTAATGGGAATGATC	3540
Db	3481	ATAAGATTTCTCTCCATATCTGATTTTCAGATTAAGAAACAGCTTAATGGGAATGATC	3540
Oy	3541	ATGCAATCTCAGGTTTGTTCAGACACTGATGACCTGTTAGATGATGCTAAATTAAGG	3600
Db	3541	ATGCAATCTCAGGTTTGTTCAGACACTGATGACCTGTTAGATGATGCTAAATTAAGG	3600
Oy	3601	AAAGTACTACTTTTGTGTAAGATGACATTAAGSAAAGTCTGCTGTTTTTACGAAAGCG	3660
Db	3601	AAAGTACTACTTTTGTGTAAGATGACATTAAGSAAAGTCTGCTGTTTTTACGAAAGCG	3660
Oy	3661	TCCAGAAAGAGAGCTTTACAGAGGCTCTAGGCCCTTACACCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGAGAGCTTTACAGAGGCTCTAGGCCCTTACACCATACACATTTGGCTCAGG	3720
Oy	3721	GTACCGAAGAGGGGCCAAGAAATTAAGACTCTCAGAGAGAACTTATCTTAGAGATG	3780

Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGATCTCAGAGAGAACTTATCTAGTAGAGATG 3780
QY 3781 AAGAGCTTCCTGCTCCAAACCTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCTGCTCCAAACCTTGTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
QY 3841 CTACTAGCATTAGCACCCTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900
Db 3841 CTACTAGCATTAGCACCCTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900
QY 3901 TATCATTTGAAGATAGCTTTAAATGATCTGAGTAAACAGGTAAATTTGGCAAAGGCATCTC 3960
Db 3901 TATCATTTGAAGATAGCTTTAAATGATCTGAGTAAACAGGTAAATTTGGCAAAGGCATCTC 3960
QY 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGTAGCTTGTCTTCAAGTGA 4020
Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGTAGCTTGTCTTCAAGTGA 4020
QY 4021 GTGATTTGGAAGACTTGTACTGCAAAATACAAACCCAGATCCCTTCTTGTATTTGTTCTT 4080
Db 4021 GTGATTTGGAAGACTTGTACTGCAAAATACAAACCCAGATCCCTTCTTGTATTTGTTCTT 4080
QY 4081 CCAAAACAATGAGGCATCAGTCTGAAACCCAGAGAGTTGGTCTGAGTGAACAAGAAATGG 4140
Db 4081 CCAAAACAATGAGGCATCAGTCTGAAACCCAGAGAGTTGGTCTGAGTGAACAAGAAATGG 4140
QY 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAGACCAAGCA 4200
Db 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAGACCAAGCA 4200
QY 4201 TGGATTCAAACTTATGAGTGAAGCAGCATCTGGGTGTGAGTGAACAAGAGTCTCTGAG 4260
Db 4201 TGGATTCAAACTTATGAGTGAAGCAGCATCTGGGTGTGAGTGAACAAGAGTCTCTGAG 4260
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGGATACCATGC 4320
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCTCAGCAGAGGGATACCATGC 4320
QY 4321 AACATTAACCTGATTAAGGCTCAGAGAGAAATGGCTGAACCTGAAGCTGTTGAACAGC 4380
Db 4321 AACATTAACCTGATTAAGGCTCAGAGAGAAATGGCTGAACCTGAAGCTGTTGAACAGC 4380
QY 4381 ATGGAGCCAGCCTTCTTCAAGCTACCTTCAATCATATGATGACTCTTCTGCCCCTTGAG 4440
Db 4381 ATGGAGCCAGCCTTCTTCAAGCTACCTTCAATCATATGATGACTCTTCTGCCCCTTGAG 4440
QY 4441 ACCCTGCGAAATCCAGAAACAAGCACAATCAGAAAAAGCAGATTTTCAACAGAAAAATG 4500
Db 4441 ACCCTGCGAAATCCAGAAACAAGCACAATCAGAAAAAGCAGATTTTCAACAGAAAAATG 4500
QY 4501 GTGAATTAACCTTATTAAGCCAAATCCAGAAAGCCCTTCTGCTGCAAGTTTGAAGTGTG 4560
Db 4501 GTGAATTAACCTTATTAAGCCAAATCCAGAAAGCCCTTCTGCTGCAAGTTTGAAGTGTG 4560
QY 4561 CAGATAGTTCTACCAAGTAAATAAAGAACAGAGAGTGAAGAGTCACTCCCTTTCTTAAT 4620
Db 4561 CAGATAGTTCTACCAAGTAAATAAAGAACAGAGAGTGAAGAGTCACTCCCTTTCTTAAT 4620
QY 4621 GCCCATCATTAATGATAGTGTGATGACATGCAAGTTGCTCTGGAAGTCTTCAAGATGA 4680
Db 4621 GCCCATCATTAATGATAGTGTGATGACATGCAAGTTGCTCTGGAAGTCTTCAAGATGA 4680
QY 4681 ACTTACCATTCTCAAGAGAGCTCATTAAGTTGATATGAGAGAGCAACAGCTGGAAG 4740
Db 4681 ACTTACCATTCTCAAGAGAGCTCATTAAGTTGATATGAGAGAGCAACAGCTGGAAG 4740
QY 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTTCGCAAGAGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTTCGCAAGAGCAAGATCTAGAGGAA 4800
QY 4801 CCCCTTAACTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTGGAATCTGATCTTCTG 4860
Db 4801 CCCCTTAACTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTGGAATCTGATCTTCTG 4860

QY 4861 AAGACAGAGCCCGAGGTGAGTCTGTGTTGGCAACATACCATCTCAACCTGTGATTA 4920
Db 4861 AAGACAGAGCCCGAGGTGAGTCTGTGTTGGCAACATACCATCTCAACCTGTGATTA 4920
QY 4921 AAGTTCGCCAATTTGAAGTTGACGAATCTGCCAGAGTCCAGCTGCTCATTAATG 4980
Db 4921 AAGTTCGCCAATTTGAAGTTGACGAATCTGCCAGAGTCCAGCTGCTCATTAATG 4980
QY 4981 ATATCTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAAAGCCGAATTTGAC 5040
Db 4981 ATATCTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAAAGCCGAATTTGAC 5040
QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGTTGGTGTCTGAGCTGACCCGAGAG 5100
Db 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGTTGGTGTCTGAGCTGACCCGAGAG 5100
QY 5101 AATTTATGCTCGTATCAAGTTTGCAGAAACACCAATCACTTTAATCTTAATTA 5160
Db 5101 AATTTATGCTCGTATCAAGTTTGCAGAAACACCAATCACTTTAATCTTAATTA 5160
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAACGAGAC 5220
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAACGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTATGCTATTTCTGGGTGACC 5280
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGGAAATGGGTAGTATGCTATTTCTGGGTGACC 5280
QY 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATATTTTGAATCAGAGAGATGTG 5340
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATATTTTGAATCAGAGAGATGTG 5340
QY 5341 TCAATGGAAGAAACCAACAGTCCAAAGGAGCAAGATTCACGAGACAGAAATCT 5400
Db 5341 TCAATGGAAGAAACCAACAGTCCAAAGGAGCAAGATTCACGAGACAGAAATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTGCTATGAGGCCCCCTTCAACAATGCCACAGATCACTG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTGCTATGAGGCCCCCTTCAACAATGCCACAGATCACTG 5460
QY 5461 AATGATGATACAGCTGTGTGCTTCTGTGTGAAGAGCTTTGATCATTAACCCCTG 5520
Db 5461 AATGATGATACAGCTGTGTGCTTCTGTGTGAAGAGCTTTGATCATTAACCCCTG 5520
QY 5521 GCAAGGTGTCCACCAATTTGTGTTGTGACAGCAATGCTTGAACAAGAGCAATGGCT 5580
Db 5521 GCAAGGTGTCCACCAATTTGTGTTGTGACAGCAATGCTTGAACAAGAGCAATGGCT 5580
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGACCCGAGAGTGGGTGGACA 5640
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGACCCGAGAGTGGGTGGACA 5640
QY 5641 GTGTAGCACTTACAGAGTCCAGAGAGTGAACCTTATACCCAGATCCCCACA 5700
Db 5641 GTGTAGCACTTACAGAGTCCAGAGAGTGAACCTTATACCCAGATCCCCACA 5700
QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 3
AAT17493
ID AAT17493 standard; cDNA; 5914 BP.
XX
XX AAT17493;
XX AC
XX AC
DT 02-OCT-1996 (first entry)
XX
XX Mutated BRCA1 coding sequence from PM06.
XX
XX Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;
KM

KM antibody production; germine alteration; probe; lesion neoplasia; human;
 KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT CDS 120..5711
 FT /tag= a
 FT /product= BRCA1 mutant
 FT mutation 2731
 FT /tag= b
 FT /note= "C to T mutation"
 XX
 XX MO9605306-A2.
 XX
 XX 22-FEB-1996.
 XX
 XX 11-AUG-1995; 95WO-US10202.
 XX
 XX 07-JUN-1995; 95US-0483553.
 XX 12-AUG-1994; 94US-0288221.
 XX 02-SEP-1994; 94US-0300266.
 XX 16-SEP-1994; 94US-0308104.
 XX 29-NOV-1994; 94US-0346824.
 XX 24-MAR-1995; 95US-0409305.
 XX 07-JUN-1995; 95US-0480784.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 XX (CMNC-) CANCER INST.
 XX (RECH-) CENT RECH DU CHUL.
 XX
 XX Durocher F, Emi M, Nakamura Y, Simard J, Shattuck-Bidens DM;
 XX
 XX WPI; 1996-139702/14.
 XX P-PSDB; AAR81535.
 XX
 XX New nucleic acid and polypeptide for mutant or polymorphic BRCA1
 XX PT gene - for diagnosis and therapy of human breast and ovarian cancer
 XX PT and for diagnosing pre-disposition to these cancers
 XX
 XX Claim 1; ; 218bp; English.
 XX
 XX AAT17439-T17453 and AAT17455-T17529 represent mutations of the human
 XX CC breast and ovarian cancer predisposing gene (BRCA1) (for wild type see
 XX CC AAT17438). Proteins encoded by these mutations (see AAR81483-R81497 and
 XX CC AAR81499-R81546) can be used as immunogens for antibody production.
 XX CC These mutant BRCA1 genes have at least 1 mutation or polymorphism in
 XX CC comparison to the wild type sequence. By detecting a germline alteration
 XX CC in the wild type BRCA1 gene, a predisposition for breast and ovarian
 XX CC cancer can be diagnosed. In one method, BRCA1 mRNA isolated from a tissue
 XX CC sample from a subject has a probe, corresponding to a fragment of the
 XX CC wild type sequence (or an allele-specific probe for one of these
 XX CC mutations), added to it. The conditions allow for hybridisation of the
 XX CC probe to the mRNA, and any hybridisation which occurs is detected.
 XX CC Alternatively the BRCA1 gene in the tissue sample is isolated, and a
 XX CC shift in electrophoretic mobility of single stranded DNA from the sample
 XX CC on a non-denaturing polyacrylamide gel indicates a mutation. These
 XX CC methods of detection can also diagnose a lesion neoplasia associated with
 XX CC the BRCA1 locus. The methods may be used in gene therapy, protein
 XX CC replacement therapy and protein mimetics, and may be used to screen for
 XX CC drugs in cancer therapy.
 XX
 XX Sequence 5914 BP; 2006 A; 1155 C; 1316 G; 1437 T; 0 other;

Query Match 100.0%; Score 5711; DB 17; Length 5914;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGAGCTTCTGAGAGCCCGGACAGGCTGTGGGTTTCCAGATAAATGAGGCC 60
 DB 1 AGCTGCTGAGAGCTTCTGAGAGCCCGGACAGGCTGTGGGTTTCCAGATAAATGAGGCC 60
 QY 61 CTGCGCTCAGAGAGCTTCACTCTGCTGTGGTAAGTTCATTGAAACAGAAAGAAA 120

DB 61 CTGCGCTCAGAGAGCTTCACTCTGCTGTGGTAAGTTCATTGAAACAGAAAGAAA 120
 QY 121 TGGATTATTCGCTCTTGGCGTTGAAGAAGTACAAAATGTCTAATATGCTATGCAAGAAA 180
 DB 121 TGGATTATTCGCTCTTGGCGTTGAAGAAGTACAAAATGTCTAATATGCTATGCAAGAAA 180
 QY 181 TCTTAGAGTCCCATCTGTCGGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGACC 240
 DB 181 TCTTAGAGTCCCATCTGTCGGAGTTGATCAAGAAACCTGTCTCCCAAAAGTGTGACC 240
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 DB 301 GTCTTTATGTAAGATATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTTAGTC 360
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 DB 361 AACTGTGGAAGAGCTATTTGAAAATCATTTGTGCTTTCACTTGACACAGTTTGGAGT 420
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 DB 421 ATGCAAAAGAGCTATTAATTTTCAAAAAAGAAAATTAATCTCTGTAACATCTAAAGATG 480
 QY 481 AAGTTTCTATATCCAAAGTATGGGCTACAAAACCCGCAAAAAGCTTCAAGAGT 540
 DB 481 AAGTTTCTATATCCAAAGTATGGGCTACAAAACCCGCAAAAAGCTTCAAGAGT 540
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 DB 541 AACCAGAAATCTCTCTTGGAGAAACAGCTCAAGTCACTCACTCACTCACTCACTCACT 600
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 DB 601 CTGTGAGAACTCTGAGACAAAGAGCGGATTAACCTCAAAAGAGCTCTGTCTTACATG 660
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 DB 661 AATTGGATTCGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTCGAGTGTGGAG 720
 QY 721 ATCAAGATTTGTAACAAATCAACCCCTCAAGAACAGGAGTGAATCAGTTGGATCTG 780
 DB 721 ATCAAGATTTGTAACAAATCAACCCCTCAAGAACAGGAGTGAATCAGTTGGATCTG 780
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 DB 781 CAAAAAGAGCTCTGTGAATTTTCTGAGAGGATTAACAATTAATGAATCATCATCAAC 840
 QY 841 CAGATTAATTAATTTGAACCACTGAGAACCGTCAAGCTGAGAGGATCAAGAAAGT 900
 DB 841 CAGATTAATTAATTTGAACCACTGAGAACCGTCAAGCTGAGAGGATCAAGAAAGT 900
 QY 901 ATCAGAGTATTTCTTTCAAACTGATGAGAGCCATGTGGCAAAATCTCATGCA 960
 DB 901 ATCAGAGTATTTCTTTCAAACTGATGAGAGCCATGTGGCAAAATCTCATGCA 960
 QY 961 GCTCATTAACAGATGAGAACAGAGTTTATTAATCTCACTAAAGAGATGATATAGAAA 1020
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Db 1381 AATATTCGTGTTCTTCAGAGAAAATAGACTTAATGAGCAGTATGCTCATGAGGCTTAA 1440
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Db 1441 TATGTAAAGTGAAGAGATTCACTCCAAATCAGTAGAGTAATATTGAAGACAAAATAT 1500
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Db 1501 TTGGGAAAACCTATCGGAAAGAGCAGCCTCCCACTTAAGCATGTAATCTGAATAATC 1560
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Db 1621 AATTAAGAGCATTTGTTACTGAGCCACAGATTAATACAAAGCCGCTCCCAATA 1680
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Db 1681 CAATTTGGAGATTCACAAACATCTCTGAATGATTAATCGGGAATACCAAGAGC 1740
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Qy 1801 CTATTCAGATGAGAAAATCTTAACCAATAGATCACTGAAAAAAGATTCGCTTCA 1860
Db 1801 CTATTCAGATGAGAAAATCTTAACCAATAGATCACTGAAAAAAGATTCGCTTCA 1860
Qy 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTCGAATTAATATTC 1920
Db 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTCGAATTAATATTC 1920
Qy 1921 ACAATTCAAAAGACCTTAAGAAATAGGCTGAGGAGAACTTCTTAACGAGCAATATTC 1980
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QY	3361	ATGCTATGCTTATGATTAGGGGTTTTCGACACCTGAGGCTCTATTAACAAAGTCTTCTGGAA	3420
Dp	3361	ATGCTATGCTTATGATTAGGGGTTTTCGACACCTGAGGCTCTATTAACAAAGTCTTCTGGAA	3420
QY	3421	GTAATTGTAGAGATCTGCGAAATTAATAAAGCAAGATATGAAGAAATGATGTCAGACTGTTA	3480
Dp	3421	GTAATTGTAGAGATCTGCGAAATTAATAAAGCAAGATATGAAGAAATGATGTCAGACTGTTA	3480
QY	3481	ATACAGATTTTCTCTCCATATCTGATTTTCAGATTAACCTTAAGAACGCTTATGGGAAGTATC	3540
Dp	3481	ATACAGATTTTCTCTCCATATCTGATTTTCAGATTAACCTTAAGAACGCTTATGGGAAGTATC	3540
QY	3541	ATGCATCTCAGGTTTGTCTGAGACCTGTAAGACCTGTATGATATGATGTAATGAATTAAGG	3600
Dp	3541	ATGCATCTCAGGTTTGTCTGAGACCTGTAAGACCTGTATGATATGATGTAATGAATTAAGG	3600
QY	3601	AAGATACTAGTTTGTCTGAAAAATGACATTAAGAAAGTTTGTGCTGTTTATGCAAAAACG	3660
Dp	3601	AAGATACTAGTTTGTCTGAAAAATGACATTAAGAAAGTTTGTGCTGTTTATGCAAAAACG	3660
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Dp	3661	TCCAGAAAGAGAGGCTTAGCAGAGAGCTTACGCTTTTGACCCATACACATTTGGCTCAGG	3720
QY	3721	GTTATCCGAAGAGGGGCGCAAGAAATTAGAGTCTCGAAGAGACATTATCTATGAGAGTG	3780
Dp	3721	GTTATCCGAAGAGGGGCGCAAGAAATTAGAGTCTCGAAGAGACATTATCTATGAGAGTG	3780
QY	3781	AAGAGCTTCCGCTCTCCAAACCTTGTTATTTGGTAAGTAACAATPAACCTTCTCAGT	3840
Dp	3781	AAGAGCTTCCGCTCTCCAAACCTTGTTATTTGGTAAGTAACAATPAACCTTCTCAGT	3840
QY	3841	CTACTAGGCAATAGCACCGTTGCTACCGAGTGTCTGTAAAGAACACAGAGGAAATTTAT	3900
Dp	3841	CTACTAGGCAATAGCACCGTTGCTACCGAGTGTCTGTAAAGAACACAGAGGAAATTTAT	3900
QY	3901	TATCATTTGAAGATAGCTTAAATATGACTGCAATACACAGATATATGGCAAAAGCATCTC	3960
Dp	3901	TATCATTTGAAGATAGCTTAAATATGACTGCAATACACAGATATATGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTGTGAGGAAACAAATGTTGTGCTAGCTGTGTTTCTTCAACGTGCA	4020
Dp	3961	AGGAACATCACCTTAGTGTGAGGAAACAAATGTTGTGCTAGCTGTGTTTCTTCAACGTGCA	4020
QY	4021	GTTGAATTTGGAAGACTTGAACCTGCAAAATACAAACCCACAGATCTTCTTGAATTTGTTCTT	4080
Dp	4021	GTTGAATTTGGAAGACTTGAACCTGCAAAATACAAACCCACAGATCTTCTTGAATTTGTTCTT	4080
QY	4081	CCAAACAAATGAGGATCATGTTGTAAAGCCAGGAGGTTGTCTGATGACACGAATTTGG	4140
Dp	4081	CCAAACAAATGAGGATCATGTTGTAAAGCCAGGAGGTTGTCTGATGACACGAATTTGG	4140
QY	4141	TTTTCGATGATGAAGAAAGGAGAACGGGCTTGAAAGAAATATATCAAGAAAGCAACCA	4200
Dp	4141	TTTTCGATGATGAAGAAAGGAGAACGGGCTTGAAAGAAATATATCAAGAAAGCAACCA	4200
QY	4201	TGGATTCAAACCTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGCTCTGTAAG	4260
Dp	4201	TGGATTCAAACCTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGCTCTGTAAG	4260
QY	4261	ACTGCTCAGGGGCTATCTCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGATACATGCG	4320
Dp	4261	ACTGCTCAGGGGCTATCTCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGATACATGCG	4320
QY	4321	AACATTAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGTGTGAACACGC	4380
Dp	4321	AACATTAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGTGTGAACACGC	4380
QY	4381	ATGGAGGCGAGGCTTCTTAACAGCTACCTTCCATATTAAGTACCTTCTGCGCTTGAAG	4440
Dp	4381	ATGGAGGCGAGGCTTCTTAACAGCTACCTTCCATATTAAGTACCTTCTGCGCTTGAAG	4440
QY	4441	ACCTGCGAAATCCAGAACCAAGCACATCAGAAAAAGCAGTATTTAATCTTACAGAAAAGTA	45000

Db	4441	ACCTGGAAATCCGAAACAAAGCACATAGAAAAGCGATTAACTTACAGAAAAGTA	4500
QY	4501	GTGAATACCCATATAAGCCAGAAATCCAGAAAGCCTTTCGTGACAAAGTTTAGGTGTG	4560
Db	4501	GTGAATACCCATATAAGCCAGAAATCCAGAAAGCCTTTCGTGACAAAGTTTAGGTGTG	4560
QY	4561	CAGATAGTTCTTACCGATTAATAAAGAACCAAGAGTGGAAAGGTATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTTACCGATTAATAAAGAACCAAGAGTGGAAAGGTATCCCTCTTAAT	4620
QY	4621	GCCCATCATTTAGATATAGTGTGTATCATGCAAGTGTCTGTGGAGTCTTCAGAAATAGA	4680
Db	4621	GCCCATCATTTAGATATAGTGTGTATCATGCAAGTGTCTGTGGAGTCTTCAGAAATAGA	4680
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Db	4661	ACTACCCATCTCAAGAGAGGCTCATTTAAGTTGTATGTGAGAGCAACAGCTGAAG	4740
QY	4741	AGTCGTGGCCACACGATTTGACGGAAACATCTTACTTGCCAAAGCAGATCTAGAGGAA	4800
Db	4741	AGTCGTGGCCACACGATTTGACGGAAACATCTTACTTGCCAAAGCAGATCTAGAGGAA	4800
QY	4801	CCCCTTACTTGGAATCTGGAATTCAGCCCTCTCTGATGACCCCTGAATCTATCCTCTG	4860
Db	4801	CCCCTTACTTGGAATCTGGAATTCAGCCCTCTCTGATGACCCCTGAATCTATCCTCTG	4860
QY	4861	AAGACAGAGCCCCAGAGAGTCAGCTGTGTGGCAACATACATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGAGTCAGCTGTGTGGCAACATACATCTTCAACCTCTGCATTTGA	4920
QY	4921	AAAGTCCCAATTGAAAGTTGACAGATCTGCCAGAGTCCAGCTGCTCTCATCTACTG	4980
Db	4921	AAAGTCCCAATTGAAAGTTGACAGATCTGCCAGAGTCCAGCTGCTCTCATCTACTG	4980
QY	4961	ATACGTCTGGGGATTAATGTCATATGGAAGAAAGTGAGAGGAGAGAGCCAGATTGACAG	5040
Db	4961	ATACGTCTGGGGATTAATGTCATATGGAAGAAAGTGAGAGGAGAGAGCCAGATTGACAG	5040
QY	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTGTGTCTGTGCCCTGACCCCAAG	5100
Db	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTGTGTCTGTGCCCTGACCCCAAG	5100
QY	5101	AATTTATGCTGTGTACAGATTTGCGAGAAAACACACATCATCTTAACTATCTAATTA	5160
Db	5101	AATTTATGCTGTGTACAGATTTGCGAGAAAACACACATCATCTTAACTATCTAATTA	5160
QY	5161	CTGAAGACATCAATCATGTGTGTATGAAAACAGATGCTGAGTGTGTGTGAACGGACAC	5220
Db	5161	CTGAAGACATCAATCATGTGTGTATGAAAACAGATGCTGAGTGTGTGTGAACGGACAC	5220
QY	5221	TGAAATATTTTCTAGAAATTCGGGAGGAAATGGGTAGTATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTTCTAGAAATTCGGGAGGAAATGGGTAGTATTTCTGGGTGACCC	5280
QY	5261	AGCTATTAAAGAAAGAAAATGCTGAATGACATGATTTGAAATCAGAGAGATGTGG	5340
Db	5261	AGCTATTAAAGAAAGAAAATGCTGAATGACATGATTTGAAATCAGAGAGATGTGG	5340
QY	5341	TCAATGGAAGAAACCAACAGGTCCMAAGCAGACAGAGATTCACAGACAGAAAGACT	5400
Db	5341	TCAATGGAAGAAACCAACAGGTCCMAAGCAGACAGAGATTCACAGACAGAAAGACT	5400
QY	5401	TCAGGGGCTTGAAGATCTGTGTATGAGGACCTTTCACCAACATGCCACAGATCAACTGG	5460
Db	5401	TCAGGGGCTTGAAGATCTGTGTATGAGGACCTTTCACCAACATGCCACAGATCAACTGG	5460
QY	5461	AATGATATGTAACAGGTGTGTGTCTTCTGTGTGAAGAGCTTTCATCAATCACTCTG	5520
Db	5461	AATGATATGTAACAGGTGTGTGTCTTCTGTGTGAAGAGCTTTCATCAATCACTCTG	5520
QY	5521	GCAACAGTGTCCACCAATTGTGTGTGTGACCCAGATGCTGTGACAGAGCAATGCT	5580
Db	5521	GCAACAGTGTCCACCAATTGTGTGTGTGACCCAGATGCTGTGACAGAGCAATGCT	5580

QY 961 GCTCATACAGCATGAGAACAGACGTTTATTACTCACTAAGACAGAAATGATGTGANA 1020
Db 961 GCTCATACAGCATGAGAACAGACGTTTATTACTCACTAAGACAGAAATGATGTGANA 1020
QY 1021 AGCGTGAATTCCTGTAATAAAGCAAAACAGCTGCTGTAGCAAGAGCCAACTAACAGAT 1080
Db 1021 AGCGTGAATTCCTGTAATAAAGCAAAACAGCTGCTGTAGCAAGAGCCAACTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCACAGAAAAAAGGTG 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCACAGAAAAAAGGTG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAATGAAATAGCAGAAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAATGAAATAGCAGAAACTGCCATGCT 1200
QY 1201 CAGAGAAATCTAGAGATACGTAAGATGTTCTTGTGTAACACTAATAGCAGCATTTGAGA 1260
Db 1201 CAGAGAAATCTAGAGATACGTAAGATGTTCTTGTGTAACACTAATAGCAGCATTTGAGA 1260
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QY 1321 GGGAGTCTGAATCAAAATGCGAAAGTATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GGGAGTCTGAATCAAAATGCGAAAGTATGATGATGATGATGATGATGATGATGATG 1380
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QY 1681 CAGATTTGAGAGTCAAAAG 1740
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Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTGGAATCTGATCTTCTG 4860
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Db 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGGCAACATTAACATCTTCAACCTCTGCAATTA 4920
Qy 4921 AAGTCCCGCAATTTGAAGTTGACAGATCTGCGCAGAGCCAGGCTGCTCATCTACTG 4980
Db 4921 AAGTCCCGCAATTTGAAGTTGACAGATCTGCGCAGAGCCAGGCTGCTCATCTACTG 4980
Qy 4981 ATACTGCTGGGTATATGCAATGGAAGAAATGTGAGCAGGAGAGACCAAGATTTGACAG 5040
Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAATGTGAGCAGGAGAGACCAAGATTTGACAG 5040
Qy 5041 CTTCAACGAAAGGGTCAACAAAGAAATGTCTCATGTGTGTCTGCTGAGCTTCAAGAGAG 5100
Db 5041 CTTCAACGAAAGGGTCAACAAAGAAATGTCTCATGTGTGTCTGCTGAGCTTCAAGAGAG 5100

QY 5101 AATTATGCTCGTGTACAGATTGGCAGAAAAACACATCACTTAATTAATTAATTA 5160
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 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGAGAC 5220
 DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGAGAC 5220
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 DB 5221 TGAATTTTCTAGAGAAATGGCGGAGAGAAATGGGAGTACTGATTTCTGGGTGACCC 5280
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 DB 5341 TCAATGGAAGAAACCAACCAAGGTCCAAGGAGAGAGAGAAATCCAGAGACAGAAAGATCT 5400
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 DB 5401 TCAAGGGGGCTAGAAATGTTGCTATGAGGGCCCTTCAACCAATGCCCAAGATCAACTGG 5460
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 DB 5461 AATGATGTGACAGCTGTGTGCTTCTGTGTGAAGAGAGCTTTCATCACTCCCTTG 5520
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 DB 5521 GCAAGAGTGTCCACCCCAATTTGTGTTGTGACGCAAGATGCTTGAAGAGAGAGATGCT 5580
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 DB 5581 TCCATGCAATTTGGGAGAGATGTGAGGACCACTGTGTGACCCCAAGATGCTTGGAC 5640
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 DB 5641 GTGTAGACACTCTACAGTGCAGAGAGTGCAGACCTTATCTGATACCCAGATCCCCACA 5700
 QY 5701 GCCACTACTGA 5711
 DB 5701 GCCACTACTGA 5711

RESULT 6
 AAV46458
 ID AAV46458 standard; cDNA; 5711 BP.
 AC AAV46458;
 XX
 DT 18-NOV-1998 (first entry)
 DE Human BRCA1 omi2 polymorphism #1 cDNA.
 XX
 KM BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 XX chromosome 17q; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 120..5711
 FT /*tag= a
 FT /product= "BRCA1 omi2 protein"
 FT variation 2201
 FT /*tag= b
 FT /note= "This polymorphic variation can be a C or T
 XX nucleotide"
 XX
 PN US5750400-A.
 XX
 PD 12-MAY-1998.

XX
 PF 12-FEB-1997; 97US-0798691.
 XX
 PR 12-FEB-1996; 96US-0598591.
 PR 12-FEB-1997; 97US-0798691.
 XX
 XX (ONCO-) ONCORMED INC.
 XX
 PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
 PI Schelter DB, Zeng B;
 XX
 DR MPI; 1998-296774/26.
 XX
 PT BRCA1 omi2 gene coding sequences - useful for distinguishing between
 PT polymorphisms and mutation(s) in the screening for disposition to
 PT breast or ovarian cancer
 XX
 PS Claim 2e; Page -; 54pp; English.
 XX
 CC This sequence encodes a human BRCA1 (breast and ovarian cancer
 CC predisposing gene) omi2 gene in which a polymorphic variation occurs at
 CC nucleotide 2201. This sequence and other polymorphic variations of this
 CC sequence are useful for the identification of an individual who may or
 CC may not have an increased susceptibility to breast or ovarian cancer.
 CC The sequences used identify gene changes which are due to polymorphisms,
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 CC suppressor) which is involved in genetic inheritance of cancers,
 CC especially breast and ovarian cancer. It is found at human chromosome
 CC 17q which is known to be linked to cancer susceptibility, especially
 CC breast cancer. Cells containing a mutation in this gene lose the
 CC wild-type function of BRCA1 and are more susceptible to cancers.
 CC NOTE: This sequence does not appear in the specification but has been
 CC created from the wild type BRCA1 omi2 gene represented in AAV46449.
 XX
 SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGCTGAGACTTCTGAGACCCGACAGGCTGTGGGTTCTCAGATTAATGGGCC 60
 DB 1 ACCTGCTGAGACTTCTGAGACCCGACAGGCTGTGGGTTCTCAGATTAATGGGCC 60
 QY 61 CCTGGCTAGAGAGGCTTCAACCTTCTGCTGGGTAAGTTCATTTGGAACGAAGAAA 120
 DB 61 CCTGGCTAGAGAGGCTTCAACCTTCTGCTGGGTAAGTTCATTTGGAACGAAGAAA 120
 QY 121 TGAATTATCTCTCTGCGGTTGAAGAGATGCAAAATGCTAATAGCTATGCAAGAAA 180
 DB 121 TGAATTATCTCTCTGCGGTTGAAGAGATGCAAAATGCTAATAGCTATGCAAGAAA 180
 QY 181 TCTTAGAGTGTCCATCTGTGAGATTGATCAAGAACCTGTCTCACAAGATGTGACC 240
 DB 181 TCTTAGAGTGTCCATCTGTGAGATTGATCAAGAACCTGTCTCACAAGATGTGACC 240
 QY 241 ACAATATTTTGCAAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGGGCTTCAAGT 300
 DB 241 ACAATATTTTGCAAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGGGCTTCAAGT 300
 QY 301 GTCTTTATGTAGATGATATATACCAAAAGAGGCTTACAAAGAAAGTACGATTAGTC 360
 DB 301 GTCTTTATGTAGATGATATATACCAAAAGAGGCTTACAAAGAAAGTACGATTAGTC 360
 QY 361 AACTGTTGAGAGCTATTGAAATCATTTGTGCTTTTCAAGTTGACACAGGTTTGGAGT 420
 DB 361 AACTGTTGAGAGCTATTGAAATCATTTGTGCTTTTCAAGTTGACACAGGTTTGGAGT 420
 QY 421 ATGCAACAGCTATATTTTGCAGAAAAAGAAATTAATCTCTCTGCAACCTTAAAGAGT 480
 DB 421 ATGCAACAGCTATATTTTGCAGAAAAAGAAATTAATCTCTCTGCAACCTTAAAGAGT 480
 QY 481 AAGTTCTATCATCAAGATATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540

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481 AAGTTTCATCATCCAAAGTATGGGCTACAGAAACCGTSCCAAAAGACTTTCTACAGAGTG 540
QY 541 AACCAGAAAATCTCTTCCTTGCGAGAAACAGTCTCAGTCCACTCTTAACTTTGAA 600
Db 541 AACCAGAAAATCTCTTCCTTGCGAGAAACAGTCTCAGTCCACTCTTAACTTTGAA 600
QY 601 CTGTGAGAACTCTGAGAACCAAGCAGCGGATCAACCTCAAAAGAGTCTGTCTACATG 660
Db 601 CTGTGAGAACTCTGAGAACCAAGCAGCGGATCAACCTCAAAAGAGTCTGTCTACATG 660
QY 661 AATTGGAGTCTGATTTCTTGAAGATACCGTTAATTAAGGCAATTATTCAGTGTGGAG 720
Db 661 AATTGGAGTCTGATTTCTTGAAGATACCGTTAATTAAGGCAATTATTCAGTGTGGAG 720
QY 721 ATCAAGAATTGTTACAAATCACCCCTCAAGGAAACGCGATGAAATCAGTTTGGATTCTG 780
Db 721 ATCAAGAATTGTTACAAATCACCCCTCAAGGAAACGCGATGAAATCAGTTTGGATTCTG 780
QY 781 CAAAAAAGGCTGCTGTGTAATTTCTGAGACGAGATGTAACAATACTGAACATCATCAAC 840
Db 781 CAAAAAAGGCTGCTGTGTAATTTCTGAGACGAGATGTAACAATACTGAACATCATCAAC 840
QY 841 CCAGTAATTAATGATTTGAAACACCACTGAGAACGCTGACAGTGAAGGCAATCCAGAAAGT 900
Db 841 CCAGTAATTAATGATTTGAAACACCACTGAGAACGCTGACAGTGAAGGCAATCCAGAAAGT 900
QY 901 ATCAGGGTATGTTCTGTTCAAACTTGCAATGTGAGAGCAATGTGGCAAAATCTCATGCCA 960
Db 901 ATCAGGGTATGTTCTGTTCAAACTTGCAATGTGAGAGCAATGTGGCAAAATCTCATGCCA 960
QY 961 GCTCATTAACAGATGAGAAACAGCAAGTTTATCTACTAAAGACAGATGATGTGAAA 1020
Db 961 GCTCATTAACAGATGAGAAACAGCAAGTTTATCTACTAAAGACAGATGATGTGAAA 1020
QY 1021 AAGCTGAATTTCTGTAATAAAAGCAAAACAGCTGCTTGAAGGAGCAACATTAACAGAT 1080
Db 1021 AAGCTGAATTTCTGTAATAAAAGCAAAACAGCTGCTTGAAGGAGCAACATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGATCCCAAGCAGAGAAAGAAAGTGA 1140
Db 1081 GGGCTGGAAGTAAGGAAACATGTAATGATAGGCGGATCCCAAGCAGAGAAAGAAAGTGA 1140
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGAATGAAGAGAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGAATGAAGAGAACTGCCATGCT 1200
QY 1201 CAGAGAAATCTAGAGATGTAAGATGTTCTTGATTAACACTAAATAGCAGATTCAGA 1260
Db 1201 CAGAGAAATCTAGAGATGTAAGATGTTCTTGATTAACACTAAATAGCAGATTCAGA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCCAAGATGAGAACTGTAGGTTCTGATGATCAACATGAG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCCAAGATGAGAACTGTAGGTTCTGATGATCAACATGAG 1320
QY 1321 GGGAGTCTGAATCAATGCAAGTAGCTGATGATTTGACGTTCTTAAATGAGAGTATG 1380
Db 1321 GGGAGTCTGAATCAATGCAAGTAGCTGATGATTTGACGTTCTTAAATGAGAGTATG 1380
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QY 1681 CAGATTTGGCAGTTCCAAAAGACTCCTCGTAATGATTAATCAAGGAACTTAACCAACGAG 1740
Db 1681 CAGATTTGGCAGTTCCAAAAGACTCCTCGTAATGATTAATCAAGGAACTTAACCAACGAG 1740
QY 1741 AGAATGTCTAAGTATGATTAATTAATTAATGATGATGATGATGATGATGATGATGAT 1800
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Db 2641 GGGAAAACAGCATGAAATGGAAGAAAGTGAACCTTGAATGCTCAGATTTTGCAGAAATCAT 2700
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QY 2701 TCAAGTTTCAAGCCGACATCTTGTCTGTTTCAATCCAGGAAATGACAGAGAG 2760
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DB 4021 GTGAATTTGGAAGCTTGAATCAATTAACAAACCCAGATCTTCTTGTGATTTGTTCT 4080
QY 4081 CCAAAACAAATGAGGATCACTGCAATTAACAAACCCAGATCTTCTGATGTAAGAAATGG 4140
DB 4081 CCAAAACAAATGAGGATCACTGCAATTAACAAACCCAGATCTTCTGATGTAAGAAATGG 4140
QY 4141 TTTAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200
DB 4141 TTTAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200
QY 4201 TGGATTTCAACTTGAAGTGAAGAGATCTGGGTGTGAGAGTGAACAAAGCTCTGGA 4260
DB 4201 TGGATTTCAACTTGAAGTGAAGAGATCTGGGTGTGAGAGTGAACAAAGCTCTGGA 4260
QY 4261 ACTGCTCAGGGGTATCTCTCAGAGTGAATTTAAACCTGAGAGAGGATACATTC 4320
DB 4261 ACTGCTCAGGGGTATCTCTCAGAGTGAATTTAAACCTGAGAGAGGATACATTC 4320
QY 4321 AACATTAACCTGATTAAGCTCCAGAGAAATGCTGAACCTAGAACTGTTAGAAACAGC 4380
DB 4321 AACATTAACCTGATTAAGCTCCAGAGAAATGCTGAACCTGATTAAGAACTGTTAGAAACAGC 4380
QY 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCATCATTAAGTGAATCTTCTGCTTGA 4440
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DB 4561 CAGATAGTTCTTCAAGTAAATTAAGAAACAGAGGTGAAGGATCATCCCTTCTAAT 4620
QY 4621 GCCCATCAATTAAGTATAGTGTGATCAATGCAAGTGTCTGAGAGTCTTCAAGTAA 4680
DB 4621 GCCCATCAATTAAGTATAGTGTGATCAATGCAAGTGTCTGAGAGTCTTCAAGTAA 4680
QY 4681 ACTACCAATCTCAAGAGAGCTCATTAAGGTTGTGATGTGAGAGAGCAACAGCTGGA 4740
DB 4681 ACTACCAATCTCAAGAGAGCTCATTAAGGTTGTGATGTGAGAGAGCAACAGCTGGA 4740
QY 4741 AGCTGGGCAACGATTTGACGGAACATCTTACCCAAAGGCAAGATCTTAGAGGAA 4800
DB 4741 AGCTGGGCAACGATTTGACGGAACATCTTACCCAAAGGCAAGATCTTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTGAGAGCCCTGAATCTGATCTCTG 4860
DB 4801 CCCCTTACCTGGAATCTGGAATCAAGCTCTTCTGAGAGCCCTGAATCTGATCTCTG 4860
QY 4861 AAGACAGAGCCCAAGAGTCAAGTCTGTTGGCAACATCTTCAACCTTCTGATTTGA 4920


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Db      4861  AAGACAGAGCCCCAGAGTCAGTCGTTGGCAATACATCTTCAACTCTGCATTGA 4920
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Db      4921  AAGTTCCCAATTGAAGTTGCAATCTGCCAGAGTCAGCTGCTCTACTACTCTG 4980
Qy      4981  ATACTGCTGGGATTAATGCAATGGAAGAAAGTGTGAGGAGGAGGAGGAGGAGG 5040
Db      4981  ATACTGCTGGGATTAATGCAATGGAAGAAAGTGTGAGGAGGAGGAGGAGGAGG 5040
Qy      5041  CTTCAACAGAAAGGGTCAACAAAGAAATGTCAGTGTGTGTCTGCGCTGACCCG 5100
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Qy      5101  AATTATGCTGTGTGACAAAGTTGCGCAAAAACCACTACTCTTAATCTTAATTA 5160
Db      5101  AATTATGCTGTGTGACAAAGTTGCGCAAAAACCACTACTCTTAATCTTAATTA 5160
Qy      5161  CTGAAGAGACTACTGATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGGAC 5220
Db      5161  CTGAAGAGACTACTGATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGGAC 5220
Qy      5221  TGAATATATTTCTAGAAATGCGGAGAGGAAAAATGGGTAGTTAGCTAATTTCTG 5280
Db      5221  TGAATATATTTCTAGAAATGCGGAGAGGAAAAATGGGTAGTTAGCTAATTTCTG 5280
Qy      5281  AGTCTATTAAGAAAGAAAAATGCTGATGAGATGATTTTGAAGTCAAGAGAGATG 5340
Db      5281  AGTCTATTAAGAAAGAAAAATGCTGATGAGATGATTTTGAAGTCAAGAGAGATG 5340
Qy      5341  TCAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGATCCCGAGACAGAA 5400
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Qy      5401  TCAGGGGGCTAGAAATCTGTGCTATGAGCCCTTCAACCAATGCCCCAGATCAAC 5460
Db      5401  TCAGGGGGCTAGAAATCTGTGCTATGAGCCCTTCAACCAATGCCCCAGATCAAC 5460
Qy      5461  AATGATGCTGACAGTGTGTGCTCTCTGTGTGTAAGAGCTTTCATCATTCACCC 5520
Db      5461  AATGATGCTGACAGTGTGTGCTCTCTGTGTGTAAGAGCTTTCATCATTCACCC 5520
Qy      5521  GCACAGGTGTCCACCAATGTTGTTGTCACGCAAGATCCTGACAGAGAGCAATG 5580
Db      5521  GCACAGGTGTCCACCAATGTTGTTGTCACGCAAGATCCTGACAGAGAGCAATG 5580
Qy      5581  TCATGCAATTTGGGAGATGTTGTAAGCACTGTGTGTGACCCGAGAGTGGTGTG 5640
Db      5581  TCATGCAATTTGGGAGATGTTGTAAGCACTGTGTGTGACCCGAGAGTGGTGTG 5640
Qy      5641  GTGTAGCACTCTACCAAGTCCGAGAGCTGAGACACTACTGATATCCCGAGATCC 5700
Db      5641  GTGTAGCACTCTACCAAGTCCGAGAGCTGAGACACTACTGATATCCCGAGATCC 5700
Qy      5701  GCCACTACTGA 5711
Db      5701  GCCACTACTGA 5711

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RESULT 7
AAV46459
ID AAV46459 standard; cDNA; 5711 BP.

AC AAV46459;
XX
XX 18-NOV-1998 (first entry)
XX
XX Human BRCA1 omi2 polymorphism #2 cDNA.
XX
XX BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.

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XX OS Homo sapiens.
XX FH Key
XX CDS Location/Qualifiers
XX FT 120..5711
XX FT /tag= a
XX FT /product= "BRCA1 omi2 protein"
XX FT variation
XX FT 2430
XX FT /tag= b
XX FT /note= "This polymorphic variation can be a T or C
XX FT nucleotide"
XX
XX US5750400-A.
XX PN
XX PD 12-MAY-1998.
XX PF 12-FEB-1997; 97US-0798691.
XX PR 12-FEB-1996; 96US-0538591.
XX PR 12-FEB-1997; 97US-0798691.
XX PA (ONCO-) ONCORMED INC.
XX PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX PI Schelter DB, Zeng B;
XX PI WPI; 1998-296774/26.
XX DR
XX PT BRCA1 omi2 gene coding sequences - useful for distinguishing between
XX PT polymorphisms and mutation(s) in the screening for disposition to
XX PT breast or ovarian cancer
XX PS
XX Claim 2e; Page -; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi2 gene in which a polymorphic variation occurs at
XX nucleotide 2430. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer.
XX The sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome
XX 17q which is known to be linked to cancer susceptibility, especially
XX breast cancer. Cells containing a mutation in this gene lose the
XX wild-type function of BRCA1 and are more susceptible to cancers.
XX NOTE: This sequence does not appear in the specification but has been
XX created from the wild type BRCA1 omi2 gene represented in AAV46449.
XX
XX Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T; 1 other;
XX
XX Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 AGCTGCTGAGAGCTCTCTGACCCCGACAGAGCTGTGGGATTTCTCAGATTAATGAGGCC 60
Db 1 AGCTGCTGAGAGCTCTCTGACCCCGACAGAGCTGTGGGATTTCTCAGATTAATGAGGCC 60
Qy 61 CTTGGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAGTTCAATTGGAACAGAAAGAAA 120
Db 61 CTTGGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAGTTCAATTGGAACAGAAAGAAA 120
Qy 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGACAAAATGTCATTAATGCTATGACAGAAA 180
Db 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGACAAAATGTCATTAATGCTATGACAGAAA 180
Qy 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGCTCCACAAAGTGTGACC 240
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGCTCCACAAAGTGTGACC 240
Qy 241 ACATATTTTGGCAATTTTGTGATGCTGAACTTCTCAACAGAAAGGAGCTTTCACAGT 300

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Db 241 ACATATTTGCAAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAAAGGCGCTTTCACAGT 300
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Db 301 GTCCCTTATGTAAGATGATATATAACCAAAAGAGCCCTACAGAAAGTACAGATTTAGTC 360
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QY 421 ATGCAAAACAGCTATTAATTTTGCAGAAAAGAAAATACTCTCTGAACATCTTAAAGATG 480
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Db 481 AAGTTCTATCATCCAAAGATGGGCTACAGAAAACCGTGCAGAAAGACTTCTACAGATG 540
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Db 601 CTGTGGAAGTCTGAGAGCAAAAGCAGGATTAACCTCAAAAGAGCTGTCTACATG 660
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Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCACTTATTGCAAGTGGAG 720
QY 721 ATCAAGATTTGTTCAAAATCACCCCTCAAGAAACAGGATGAATCAAGTTGGATTTCTG 780
Db 721 ATCAAGATTTGTTCAAAATCACCCCTCAAGAAACAGGATGAATCAAGTTGGATTTCTG 780
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Db 781 CAAAAAAGCGCTGTTGTTGGAATTTTCTGAGACGATGTAAACAAATGATGAACATCAAC 840
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Db 1021 AGGCTGAATTTCTGTATTAATAAGCAAGCGCTGCTTAGCAGAGGACCAATTAACAGT 1080
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Db 1081 GGGCTGGAAGTGAAGAAACATGTATAGGCGGACTCCAGCAAGAAAAGAGTGA 1140
QY 1141 ATCTGAATGCTGATCCCCCTGTGTGAGAGAAAAGATGAATGAAGCAATGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCCCTGTGTGAGAGAAAAGATGAATGAAGCAATGCCATGCT 1200
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Db 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680
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Db 1681 CAGATTTGCACTTCAAAAAGTCTCTGAAATGATTAATCAGGAACTAACCAAGGAGC 1740
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Db 1741 AGAATGCTCAAGTGAATATTTACTTAATAGTGTCAATGAGATTAATAACAAAGGTATT 1800
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Db 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATGACAGAAA 180
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Db 2101 GGCACAGAGAAACCTTACAACTCATGAGAGTAAAGAACTGCAACCTGAGAGCCAAAGAGA 2160
QY 2161 GTAAACAGCCAAATGAAGACAGCAAGTAAAGACATGACAGGATACTTTCCACAGAGCTGA 2220
Db 2161 GTAAACAGCCAAATGAAGACAGCAAGTAAAGACATGACAGGATACTTTCCACAGAGCTGA 2220
QY 2221 AGTTAAACAAATGACCTGCTTCTTTTCTAAGTGTCAAAATACCAATGAATTTAAAGAT 2280
Db 2221 AGTTAAACAAATGACCTGCTTCTTTTCTAAGTGTCAAAATACCAATGAATTTAAAGAT 2280
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Db	2221	AGTTAACAAATGCACTGGTCTTTTACTAAGTGTCAAAATCCAGTGAACCTTAAAGAT	2280
QY	2281	TTGTCAATCTTACGCTTCCCAAGAGAAAGAAAAGAGAAAAGAAAAGTAAAGTGT	2340
Db	2281	TTGTCAATCTTACGCTTCCCAAGAGAAAGAAAAGAGAAAAGTAAAGTGT	2340
QY	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAGGGTTTGCAACTG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAAGAGGGTTTGCAACTG	2400
QY	2401	AAAGATCTGTAGAGGTGACAGTATTTGATTTGCTGCTGGTATCTGATTTAATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGGTGACAGTATTTGATTTGCTGCTGGTATCTGATTTAATGGCACTCAGG	2460
QY	2461	AAAGATCTCGTTACTGGAAGTTAGCACTTACGGAAGGCAAAAACAGAACCAATTAAT	2520
Db	2461	AAAGATCTCGTTACTGGAAGTTAGCACTTACGGAAGGCAAAAACAGAACCAATTAAT	2520
QY	2521	GTGTAGTCAGTGTCAGACATTTGAAAACCCAAGGACCTAATTCATGTTGTTCCAAG	2580
Db	2521	GTGTAGTCAGTGTCAGACATTTGAAAACCCAAGGACCTAATTCATGTTGTTCCAAG	2580
QY	2581	ATTAATGAAATGACACAGAAGGCTTTAAGTATCCATTGGACATGAAGTTAACACAGTC	2640
Db	2581	ATTAATGAAATGACACAGAAGGCTTTAAGTATCCATTGGACATGAAGTTAACACAGTC	2640
QY	2641	GGGAACACAGCATTAAGAAATGGAAGAAAGTGAACCTGATGCTCAGATTTGCAAAATCAT	2700
Db	2641	GGGAACACAGCATTAAGAAATGGAAGAAAGTGAACCTGATGCTCAGATTTGCAAAATCAT	2700
QY	2701	TCGAAGTTTCAAAAGGCCAGTCATTTGCTGTGTTTCCAAATCCAGAAATCCAGAAGNG	2760
Db	2701	TCGAAGTTTCAAAAGGCCAGTCATTTGCTGTGTTTCCAAATCCAGAAATCCAGAAGNG	2760
QY	2761	AATGTGCAACATTTCTTGGCCCACTGTGGTCTTTAAGAAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTTGGCCCACTGTGGTCTTTAAGAAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAAGAGTCTAATTCGAAGCTGATC	2880
Db	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAAGAGTCTAATTCGAAGCTGATC	2880
QY	2881	AGACAGTTAATATCACTGACAGGCTTCTGTGTGTGTGCACAAGAAATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGACAGGCTTCTGTGTGTGTGCACAAGAAATAGCCAGTTGATA	2940
QY	2941	ATGCCAAATGTATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCCAAATGTATATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA	3000
QY	3001	ACGAATCTGAGACTCTTACTCCAAATTAACATGACTTTTACAAACCCCATATGTATAC	3060
Db	3001	ACGAATCTGAGACTCTTACTCCAAATTAACATGACTTTTACAAACCCCATATGTATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAAGAAAATCTGCTAGAG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAATGTAAAGAAAATCTGCTAGAG	3120
QY	3121	AAAACTTTGAGAACATTCATTCATGCTCACTGAAAAGAAATGGGAAATGAGAACATTCOA	3180
Db	3121	AAAACTTTGAGAACATTCATTCATGCTCACTGAAAAGAAATGGGAAATGAGAACATTCOA	3180
QY	3181	GTACAGTGAACAATTAGCCGTAATACATTAAGAGAAAATGTTTTTAAGAACCCAGCT	3240
Db	3181	GTACAGTGAACAATTAGCCGTAATACATTAAGAGAAAATGTTTTTAAGAACCCAGCT	3240
QY	3241	CAAGCAATTAATTAAGATAGGTTCCACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATTAATTAAGATAGGTTCCACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
QY	3301	TAGGTTCAAGTGATGAAAACTTCAAGCAAACTTAGTGAACAAGGGCCAAAATTTGA	3360
Db	3301	TAGGTTCAAGTGATGAAAACTTCAAGCAAACTTAGTGAACAAGGGCCAAAATTTGA	3360

Db	3301	AAGGTTCCAGTGAATGAAAAACCTTACAGCAKAACTAGTGAAGAAACAGAGGGCCAAATTTGA	3360
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Db	3361	ATGCTATGCTTAGATTAGAGGGTTTTTGCAACCTGAGGCTATATMAACAAAGTCTTCTGGAA	3420
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Db	3421	GTAATTGTAGACATCTCTGAATTAATAAAGCAAGAAATATGAAGAAGTAGTTCAGACTGTTA	3480
Qy	3481	ATACAGATTTCTCCATCATCTGATGATTTTCAGATTAACCTTAGAACACGCTATGGGAAGTATGC	3540
Db	3481	ATACAGATTTCTCCATCATCTGATGATTTTCAGATTAACCTTAGAACACGCTATGGGAAGTATGC	3540
Qy	3541	ATGCATCTCAGGTTTGTTCTGAGACACCTGATGACCTGTGTAGATGATGATGATTAAGAAG	3600
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Qy	3661	TCCAGAAAGGAGACCTTAGCAGAGAGTCCCTACCCCTTTCACCCATACACTTTGGCTCAGG	3720
Db	3661	TCCAGAAAGGAGACCTTAGCAGAGAGTCCCTACCCCTTTCACCCATACACTTTGGCTCAGG	3720
Qy	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGAGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGAGAGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCACACGTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACACGTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCAATAGACCCGTGTGCTACCCAGATGCTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCAATAGACCCGTGTGCTACCCAGATGCTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTAAAGAAATAGCTTAATAATAGCTAGCACTAACCGAGTAAATTTGGCAAAAGCATCTC	3960
Db	3901	TATCATTTAAAGAAATAGCTTAATAATAGCTAGCACTAACCGAGTAAATTTGGCAAAAGCATCTC	3960
Qy	3961	AGGAACATCACCTTAGTGAGGAAACAAATGTTCGTAGCTTTTCTTACAGTGCA	4020
Db	3961	AGGAACATCACCTTAGTGAGGAAACAAATGTTCGTAGCTTTTCTTACAGTGCA	4020
Qy	4021	GTGAATTGGAAAGACTTGACCTGCAAAATACAAACCCAGAGATCCCTTCTTGATTTGGTCTTT	4080
Db	4021	GTGAATTGGAAAGACTTGACCTGCAAAATACAAACCCAGAGATCCCTTCTTGATTTGGTCTTT	4080
Qy	4081	CCAAACAAATAGGCACTAGCTGTGAAGACCGAGAGTTGGCTGTAGTGACAAAGAAATTTGG	4140
Db	4081	CCAAACAAATAGGCACTAGCTGTGAAGACCGAGAGTTGGCTGTAGTGACAAAGAAATTTGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAAAGCA	4200
Qy	4201	TGGAATTCAAACTTAGTGGAAGCAGACATCTGGGTGTGAGATGAAACAAAGCTCTCTGAAG	4260
Db	4201	TGGAATTCAAACTTAGTGGAAGCAGACATCTGGGTGTGAGATGAAACAAAGCTCTCTGAAG	4260
Qy	4261	ACTGCTCAGGGCTATCCCTCTAGGTACATTTTAAACCACTCAGCAAGAGGATATCAATGC	4320
Db	4261	ACTGCTCAGGGCTATCCCTCTAGGTACATTTTAAACCACTCAGCAAGAGGATATCAATGC	4320
Qy	4321	AACATTAACCTGATTAAGGCTCCAGCAGAGAAATGGCTGAATCTAGAAAGCTGTGTTAAGACAG	4380
Db	4321	AACATTAACCTGATTAAGGCTCCAGCAGAGAAATGGCTGAATCTAGAAAGCTGTGTTAAGACAG	4380
Qy	4381	ATGGAGCAGACCTTTCTPAACAGCTACCCCTTTCATATAGTACTCTTTCTGCCCTTAGAG	4440
Db	4381	ATGGAGCAGACCTTTCTPAACAGCTACCCCTTTCATATAGTACTCTTTCTGCCCTTAGAG	4440

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 DB 4561 CAGATAGTTCTACCGATAAAAATTAAGAACCGAGAGTGAAGAGTCATCCCTCTTAAT 4620
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 DB 4621 GCCCATCTTATGATATGATAGTGTGTCATGACAGATTTGCTGAGAGTCTTCAAGATAGAA 4680
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 DB 4741 AGTCTGGGCGCACAGATTTGACGGAACAATCTTACTTCCAGAGCAAGATCTAGAGGAA 4800
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 QY 4921 AAGTTCCTCCATTTGAAGTTGCGAATCTGCCAGAGTCCAGCTGTCTCATCTACG 4980
 DB 4921 AAGTTCCTCCATTTGAAGTTGCGAATCTGCCAGAGTCCAGCTGTCTCATCTACG 4980
 QY 4981 ATACTGCTGGGATATATGCAATGGAAGAAAGTGTGAGGAGGAGAACAGAAATGACAG 5040
 DB 4981 ATACTGCTGGGATATATGCAATGGAAGAAAGTGTGAGGAGGAGAACAGAAATGACAG 5040
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QY 5521 GCACAGGTGTCCACCAATTTGTTGTGTCAGCCAGATGCTGTGACAGAGACATGCT 5580
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 QY 5701 GCCACTACTGA 5711
 DB 5701 GCCACTACTGA 5711

RESULT 9
 AAV46461
 ID AAV46461 standard; cDNA; 5711 BP.
 XX
 AC AAV46461;
 XX
 DT 18-NOV-1998 (first entry)
 XX
 DE Human BRCA1 omi2 polymorphism #4 cDNA.
 XX
 KW BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
 OS chromosome 17q; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 120..5711
 FT /*tag= a
 FT /product= "BRCA1 omi2 protein"
 FT variation 3232
 FT /tag= b
 FT /note= "This polymorphic variation can be an A or G nucleotide"
 FT
 PN US5750400-A.
 XX
 PD 12-MAY-1998.
 XX
 PF 12-FEB-1997; 97US-0798691.
 XX
 PR 12-FEB-1996; 96US-0538591.
 PR 12-FEB-1997; 97US-0798691.
 XX
 PA (ONCO-) ONCORMED INC.
 XX
 PI Allen AC, Alvares CP, Citz BS, Murphy PD, Olson SJ;
 PI Schelter DB, Zeng B;
 XX
 DR WPI; 1998-296774/26.
 XX
 PT BRCA1 omi gene coding sequences - useful for distinguishing between
 PT polymorphisms and mutation(s) in the screening for disposition to
 PT breast or ovarian cancer
 XX
 PS Claim 2e; Page -; 54pp; English.
 CC This sequence encodes a human BRCA1 (breast and ovarian cancer
 CC predisposing gene) omi2 gene in which a polymorphic variation occurs at
 CC nucleotide 3232. This sequence and other polymorphic variations of this
 CC sequence are useful for the identification of an individual who may or
 CC may not have an increased susceptibility to breast or ovarian cancer.
 CC The sequences used identify gene changes which are due to polymorphisms,
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
 CC suppressor) which is involved in genetic inheritance of cancers,
 CC especially breast and ovarian cancer. It is found at human chromosome

Db	4261	ACTGCTAGGGGCTATCCCTCTCAGAGTGACATTTTAAACCACCTCAGACAGAGGATACATGTC	4320
Oy	4321	AACATTAACCTGATTAAGTCCAGCAGGAAATGCTGAACCTAGAGCTGTGTTAGAACAC	4380
Db	4321	AACATTAACCTGATTAAGTCCAGCAGGAAATGCTGAACCTAGAGCTGTGTTAGAACAC	4380
Oy	4381	ATGGAGGCACGCTTCTTAACAGCTACCCCTTCATCATTAAGAGACTCCCTGCTGAGG	4440
Db	4381	ATGGAGGCACGCTTCTTAACAGCTACCCCTTCATCATTAAGAGACTCCCTGCTGAGG	4440
Oy	4441	ACCTGCGAAATCCAGAACAAAGCATCAGAAAAAGCAGATTAACTTCACAGAAAAATA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCATCAGAAAAAGCAGATTAACTTCACAGAAAAATA	4500
Oy	4501	GTGAATACCCCTATTAAGCCAGAAATCCAGAAAGCCTTTCCTGTCGACAAAGTTGAGGTGCTG	4560
Db	4501	GTGAATACCCCTATTAAGCCAGAAATCCAGAAAGCCTTTCCTGTCGACAAAGTTGAGGTGCTG	4560
Oy	4561	CAGATAGTCTTACACAGTAAAAATAAGAACCCAGAGTGGAAAGGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTCTTACACAGTAAAAATAAGAACCCAGAGTGGAAAGGTCAATCCCTCTTAAT	4620
Oy	4621	GCCCATCTTATGATATATGCTGTATCATGCACAGTTGCTCTGGAGATCTTAAATAGAA	4680
Db	4621	GCCCATCTTATGATATATGCTGTATCATGCACAGTTGCTCTGGAGATCTTAAATAGAA	4680
Oy	4681	ACTACCCTATCCAGAGAGAGCTCATTTAAGTTGTGATGTGGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTACCCTATCCAGAGAGAGCTCATTTAAGTTGTGATGTGGAGAGCAACAGCTGGAAG	4740
Oy	4741	AGTCTGGGCCACACGATTGACGGAAACATCTTACTTCCAGGCAAGATCTAAGAGAA	4800
Db	4741	AGTCTGGGCCACACGATTGACGGAAACATCTTACTTCCAGGCAAGATCTAAGAGAA	4800
Oy	4801	CCCCCTACTGGAATCTGGAATPCAGGCCCTTCTCGTAGAACCTCGAATCTGATCCCTCTG	4860
Db	4801	CCCCCTACTGGAATCTGGAATPCAGGCCCTTCTCGTAGAACCTCGAATCTGATCCCTCTG	4860
Oy	4861	AAGACAGAGCCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCCAACTCTGCATTTGA	4920
Db	4861	AAGACAGAGCCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCCAACTCTGCATTTGA	4920
Oy	4921	AAGTTTCCCATTTGAAAGTTGACAAATCTGCCAGGGTCCAGCTGTGCTCATACTACTG	4980
Db	4921	AAGTTTCCCATTTGAAAGTTGACAAATCTGCCAGGGTCCAGCTGTGCTCATACTACTG	4980
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Db	4981	ATACTGCTGGGTATATATGCAATGGAAGAAATGTGAGCAGGAGAGACCAAAATTGACAG	5040
Oy	5041	CTTCAACAAGAAAGGCTCAACAAMAGATGTCATGTGTGTCTGAGCTTGACCCCAAGAG	5100
Db	5041	CTTCAACAAGAAAGGCTCAACAAMAGATGTCATGTGTGTCTGAGCTTGACCCCAAGAG	5100
Oy	5101	AATTATGCTGTGTACAAAGTTTGGCAGAAAACCAATCATCTTAACTTAATCTAATTTA	5160
Db	5101	AATTATGCTGTGTGTACAAAGTTTGGCAGAAAACCAATCATCTTAACTTAATCTAATTTA	5160
Oy	5161	CTGAAGAGACTACTCATGTTGTATTGAAAAAGATGCTGAATTTGTGTGTAACGACAC	5220
Db	5161	CTGAAGAGACTACTCATGTTGTATTGAAAAAGATGCTGAATTTGTGTGTAACGACAC	5220
Oy	5221	TGAAATATTTTCTAGGAATGCGGAGAGAAATGGGTGTTAGCTAATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTTCTAGGAATGCGGAGAGAAATGGGTGTTAGCTAATTTCTGGGTGACCC	5280
Oy	5281	AGCTATTATTAAGAAAGAAATGCTGAAATGAGCATGATTTTGAATCAGAGAGATGTGG	5340
Db	5281	AGCTATTATTAAGAAAGAAATGCTGAAATGAGCATGATTTTGAATCAGAGAGATGTGG	5340
Oy	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGCGACAAAGAAATCCAGACAGAAAGATCT	5400

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Db      5341 TCATGGAAGAAACCAACCAAGGTCCTCAAGCGAGCAAGATCCACAGACAGAAAGATCT 5400
Oy      5401 TCAGGGGGCTAGAAATCTGTTCGTATGAGCCCTTCACCAACATGCCACAGATCAACTGG 5460
Db      5401 TCAGGGGGCTAGAAATCTGTTCGTATGAGCCCTTCACCAACATGCCACAGATCAACTGG 5460
Oy      5461 AATGATGATGTAACAGCTGTGTGTGCTTCTGTGTGAAGAGACTTTCATTCATCCCTTG 5520
Db      5461 AATGATGATGTAACAGCTGTGTGTGCTTCTGTGTGAAGAGACTTTCATTCATCCCTTG 5520
Oy      5521 GCACAGGTGTCCACCCATTTGTGTGTGTGCACGCAATGCCCTGCACAGAGACATGTGCT 5580
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RESULT 2
US-08-798-691-1
; Sequence 1, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antoinette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Galchtersberg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,691
; FILING DATE: 12-Feb-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Gallegos
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: PA-0054CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2051
; TELEFAX: 301-208-6997
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
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QY 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940
QY 2941 ATGCAAAATGTAGATCAAGAGAGGCTGTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000
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QY 3181 GTACAGTAGACCAATTAAGCCGTAAATAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240
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QY 4201 TGGATTCAAACTTAAGTGAAGAGCAGCATCTGGGGTGAAGTGAAGTGAAGCAACGCTCTGAG 4260
Db 4201 TGGATTCAAACTTAAGTGAAGAGCAGCATCTGGGGTGAAGTGAAGTGAAGCAACGCTCTGAG 4260
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MAP POSITION: 17q21
US-08-598-591-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGGTGAGACTTCTGACACCCCGACAGAGGTGGGTTCTCAGATTAATCGGCC 60
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DB 481 AAGTTTATATCTCAAAAGATATGGGCTACAGAAACCGTCCAAAAGCTTCTACAGATG 540
QY 541 AACCCGAAAATCCCTCTGAGAGAAACAGTCTCAGTGTCAACTCTAACTTGAAG 600
DB 541 AACCCGAAAATCCCTCTGAGAGAAACAGTCTCAGTGTCAACTCTCTTGAAG 600
QY 601 CTGTGAGAACTCTGAGAGCAAGAGCAGGATACAACTCAAAAAGACGTCTGTACATTTG 660
DB 601 CTGTGAGAACTCTGAGAGCAAGAGCAGGATACAACTCAAAAAGACGTCTGTACATTTG 660
QY 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATGCACTGTGGAG 720
DB 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATGCACTGTGGAG 720
QY 721 ATCAAGAAATGTTAACAATGACCCCTCAAGGAAACAGAGATGAATAGTTGGATCTG 780
DB 721 ATCAAGAAATGTTAACAATGACCCCTCAAGGAAACAGAGATGAATAGTTGGATCTG 780
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTACAAATATCTGAACATCATAC 840
DB 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTACAAATATCTGAACATCATAC 840
QY 841 CCAAGTAATATGATTTGAACACCACTGAGAAAGCTGCACTGAGAGGATTCAGAAAAGT 900
DB 841 CCAAGTAATATGATTTGAACACCACTGAGAAAGCTGCACTGAGAGGATTCAGAAAAGT 900
QY 901 ATCAGGAGTATGTTCTTCAAACTTGCATGTGAGAGGATGAGCAAAATATCTATGCCA 960
DB 901 ATCAGGAGTATGTTCTTCAAACTTGCATGTGAGAGGATGAGCAAAATATCTATGCCA 960
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QY 1681 CAGATTTGGCAGTTCAAAAAGACTCTGGAATGATTAATCAGGGAATTAACCAACGAGGC 1740
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QY 1741 AGAATGCTCAAGTATGATTAATTAATAGTGTCTATGGAATTAACCAAAAGGTGATT 1800
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QY 1801 CTATTGCAATGAGAAAATCTTAACCCATGATCATCTGAGAAAAGAAATCTGCTTTCA 1860
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QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGAGTAAAGCAATATGAACTGAAATTAATATCC 1920
DB 1861 AAAAGAAAGCTGAACCTATTAAGCAGAGTAAAGCAATATGAACTGAAATTAATATCC 1920
QY 1921 ACAATTTCAAAAGCACTTAAGAAATATGCTGAGAGAGAGTCTTCAACAGGCAATATTC 1980
DB 1921 ACAATTTCAAAAGCACTTAAGAAATATGCTGAGAGAGAGTCTTCAACAGGCAATATTC 1980
QY 1981 ATGCGCTTGAATAGTATGATGATTAAGCCCACTTAATTTGATGAAATTTGCAAA 2040
DB 1981 ATGCGCTTGAATAGTATGATGATTAAGCCCACTTAATTTGATGAAATTTGCAAA 2040
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAGAAAGTATCAACCAATATGCACTCA 2100
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAGAAAGTATCAACCAATATGCACTCA 2100

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:57:10 ; Search time 283 seconds
(without alignments)
6188.802 Million cell updates/sec

Title: US-09-734-672-1

Perfect score: 5711
Sequence: 1 AGCTCGCTGAGACTTCTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

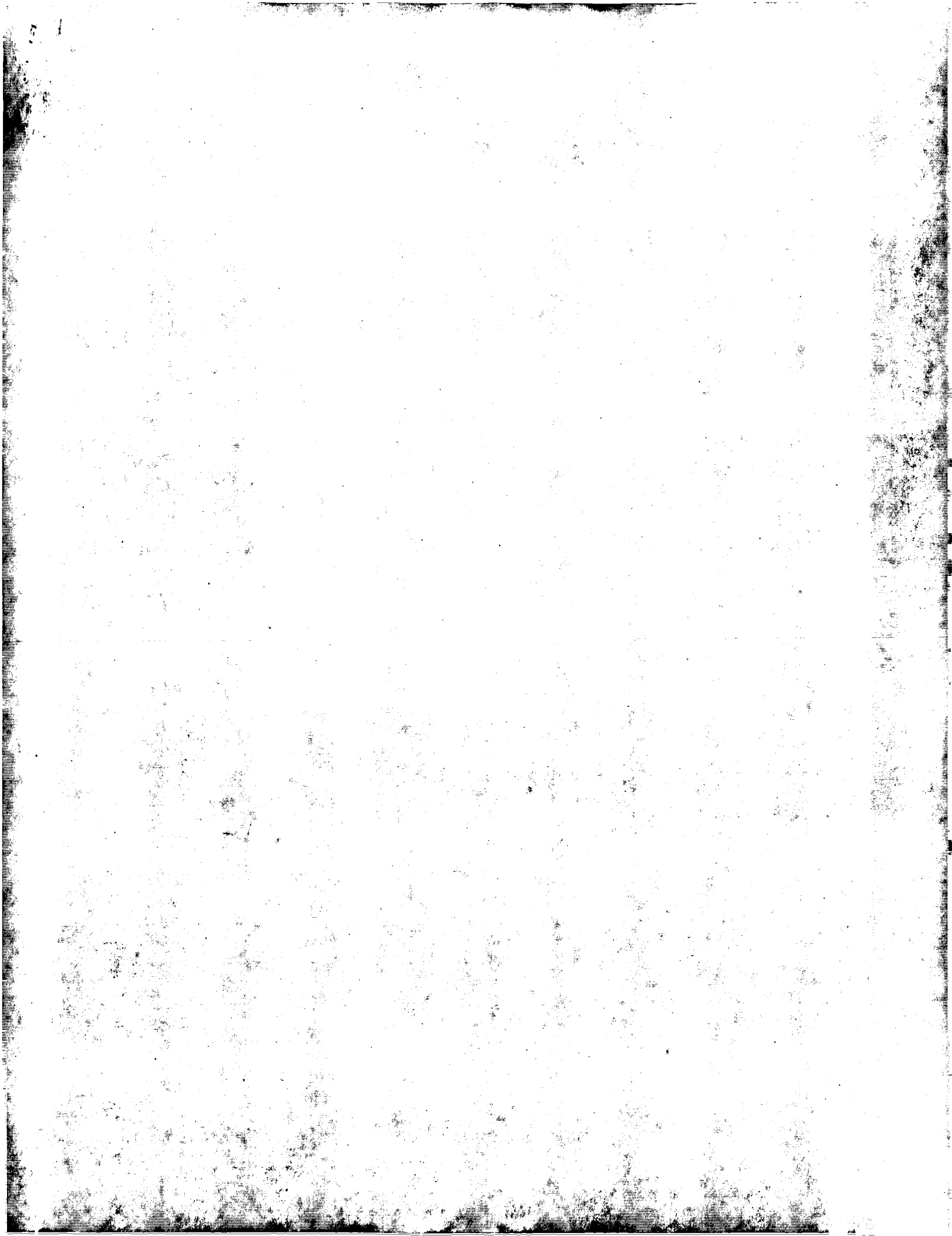
SUMMARIES

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4	5711	100.0	5711	3	US-09-074-476-1
5	5709.4	100.0	5711	1	US-08-798-691-5
6	5709.4	100.0	5711	3	US-08-825-487A-5
7	5709.4	100.0	5711	3	US-09-074-476-3
8	5701.4	99.8	5711	1	US-08-798-691-3
9	5701.4	99.8	5711	3	US-08-825-487A-3
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13	5699.8	99.8	5712	3	US-09-099-753-1
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25	5698.2	99.8	5711	1	US-08-425-061-10
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34	5685.8	99.6	5709	1	US-08-425-061-7	Sequence 7, Appli
35	5685.8	99.6	5709	1	US-08-425-061-8	Sequence 8, Appli
36	5685.8	99.6	5709	1	US-08-425-061-11	Sequence 11, Appli
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43	5645.8	98.9	5689	1	US-08-425-061-3	Sequence 3, Appli
44	5645.8	98.9	5689	1	US-08-825-886-3	Sequence 3, Appli
45	5619.6	98.4	5770	1	US-08-425-061-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-598-591-1
Sequence 1, Application US/08598591
Patent No. 5654155
GENERAL INFORMATION:
APPLICANT: Allen, Antonette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Citz, Brenda S.
APPLICANT: Murphy, Patricia D.
APPLICANT: Olson, Sheri J.
APPLICANT: Schelter, Denise B.
APPLICANT: Zeng, Bin
TITLE OF INVENTION: A Consensus Sequence of the Human BRCA1 Gene
Patent No. 5654155
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/598,591
FILING DATE: herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Swecker, Robert S.
REGISTRATION NUMBER: 19,885
REFERENCE/DOCKET NUMBER: 020160-282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17



QY 3955 CATCTCAGGAACATCAGCTTACCTAGTGAAGAAACAAATGTTCTGCTTCTTCTTCTCAG 4014
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RESULT 15
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 LOCUS 602377909F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4508450 5',
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 ACCESSION BG257190
 VERSION BG257190.1 GI:12767019
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 938)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10387 row: b column: 03
 High quality sequence stop: 657.
 Location/Qualifiers
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 /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 294 a 193 c 225 g 226 t
 ORIGIN

Query Match 11.4%; Score 651.6; DB 12; Length 938;
 Best Local Similarity 93.9%; Pred. No. 9,8e-143;
 Matches 712; Conservative 0; Mismatches 39; Indels 7; Gaps 3;

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DB 70 TCTGGGTAAAGTTCAATGGAACAGAAAGAAATGATGATTTATCTGCTTTCGCGTTGAAGAA 129
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 DB 190 ATCAAGAAACCTGTCTCCACAAAGTGTGACACATATTTTGCATTTTTCATCTGCTGAA 249
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 QY 570 AGTCTCAGTGTCAACTCTCTTAACCTTGAACCTGTGAACCTGTGAGACAAAGCAGCG 629
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 DB 607 ATACACTC---AAAGAGCTGTGTCTACATTTGAATTTGGATTTGTTCTTGAAAGATAC 663
 QY 689 CGTTAATTAAGCACTTATTCAGTGTGGGAGATCAAGAAATTTTACAAATCAACCCCTCA 748
 DB 664 CGTTAATTAAGCACTTATTTGAGTGTGGGAGATCAACAGAAATTTTCAATCAACCCCT 723
 QY 749 AGGAACCAAGGATGAATCACTTTGATTTGCAAAAA 786
 DB 724 CAGGAACAGGATGAATCAAGTGTGATCTGCGCAAAA 761

Search completed: June 13, 2003, 12:11:40
 Job time : 6809 secs

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Db      1  TTAGCTTGACACAGGTTTGAGATATGCAACAGCTATATTTTGCAGAAAAAGAAATA 60
QY      458  CTCTCTGAAACATTTAAAGATGAAGTTTCTATCATCTCAAGATATGGGCTACAGAAACCG 517
Db      61  CTCTCTGAAACATTTAAAGATGAAGTTTCTATCATCTCAAGATATGGGCTACAGAAACCG 120
QY      518  TGGCAAAAAGCTTCTACAGAGTGAACCCGAAATCCCTCTGAGAGAAACCAAGTCTCAG 577
Db      121  TGGCAAAAAGCTTCTACAGAGTGAACCCGAAATCCCTCTGAGAGAAACCAAGTCTCAG 177
QY      578  TGTCCAACTCTCTAACCTTGGAACCTGTGAGAACTCTGAGAACAAAGCAGCGATACAC 637
Db      178  TGTCCAACTCTCTAACCTTGGAACCTGTGAGAACTCTGAGAACAAAGCAGCGATACAC 237
QY      638  TCAAAAAGAGCTCTGTCTACATTTGAATTGGGATCTGATCTTCTGAGATACCGTTAATA 697
Db      238  TCAAAAAGAGCTCTGTCTACATTTGAATT----- 264
QY      698  GGCAACTTATGTGAGTGGAGATCAAGATTTGTACAATCACCCTCAGGAACGAG 757
Db      265  ----- 264
QY      758  GGATGAATATGATTTGATTTCTGCAGAAAAAGGCTGCTGTGAATTTTCTGAGACGATGT 817
Db      265  -----GGCTGCTTGTGAATTTTCTGAGACGATGT 294
QY      818  AACCAATATCTGACATCATCAACCAATATATGATTTGACACCACTGAGAAACGCTGC 877
Db      295  AACCAATATCTGACATCATCAACCAATATATGATTTGACACCACTGAGAAACGCTGC 354
QY      878  AGCTGAGAGGATCCAGAAAAAGTATCAAGGAGTCTGTTCAAACTGATGAGAGGAGCC 937
Db      355  AGCTGAGAGGATCCAGAAAAAGTATCAAGGAGTCTGTTCAAACTGATGAGAGGAGCC 414
QY      938  ATGTGACACAAATATCTGATGCGACCTGATTAACAGCATGAGAACAGCAGTTTATTACTAC 997
Db      415  ATGTGACACAAATATCTGATGCGACCTGATTAACAGCATGAGAACAGCAGTTTATTACTAC 474
QY      998  TTAAGACAGATGATATGTAAGAAAGGCTGATTTCTGTATTAAGGAAACAGCCTGCTT 1057
Db      475  TTAAGACAGATGATATGTAAGAAAGGCTGATTTCTGTATTAAGGAAACAGCCTGCTT 534
QY      1058  AGCAAGAGGCAACATTAACAGATGAGGCTGAGAGTGAAGAAACATGATATGAGAGCGAC 1117
Db      535  AGCAAGAGGCAACATTAACAGATGAGGCTGAGAGTGAAGAAACATGATATGAGAGCGAC 594
QY      1118  TCCGAGCAGAAAAAGGATGATCTGAATGCTGATCCCTGTGTGAGAGAAAGATG 1177
Db      595  TCCGAGCAGAAAAAGGATGATCTGAATGCTGATCCCTGTGTGAGAGAAAGATG 654
QY      1178  GAATTAAGCAGAAATCTGCCATGCTCAGAGAACTCTAGAGATCTGAAGATGTTCTTGAT 1237
Db      655  GAATTAAGCAGAAATCTGCCATGCTCAGAGAACTCTAGAGATCTGAAGATGTTCTTGAT 714
QY      1238  AACCTAAATATGAGCAGATTCAGAAAGTTAATGAGTGTTCCTGAGAGTGAAGTGT 1297
Db      715  AACCTAAATATGAGCAGATTCAGAAAGTTAATGAGTGTTCCTGAGAGTGAAGTGT 774
QY      1298  AGGTTCTGATGATCTCAGATGATGGGAGTCTGAATCAAAATGCAAGATGCT-GATGTAT 1356
Db      775  AGGTTCTGATGATCTCAGATGATGGGAGTCTGAATCAAAATGCAAGATGCTGATGTAT 834
QY      1357  TGAACGTT-CTTAATGAGTATGATG---AATATCTGTGTTCTTCAAGAAATATGACTT 1411
Db      835  TGAACGTTCTTAATGAGTATGATGATATTTCTTTCAGAGAAATATGACTT 893

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RESULT 14
LOCUS   BF791668          900 bp      mRNA      linear      EST 12-JAN-2001
DEFINITION  602251822P1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4344317 5',
            mRNA sequence.
ACCESSION  BF791668

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VERSION BF791668.1 GI:12096722
KEYWORDS EST
SOURCE  human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS   NIH-MGC http://mgs.nci.nih.gov/.
TITLES    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          plate: LLAM9962 row: k column: 06
          High quality sequence stop: 678.
FEATURES
     source
         1. 900
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:4344317"
            /issue_type="adrenal cortex carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site: 1;
            Note: Site 2: Salt; Cloned unidirectionally; oligo-dT
            primed. Average insert size 1.229 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: This is a NIH_MGC library."
BASE COUNT  283 a 176 c 212 g 229 t
ORIGIN
Query Match 11.5%; Score 657; DB 12; Length 900;
Best Local Similarity 96.5%; Pred. No. 5.1e-144;
Matches 736; Conservative 0; Mismatches 20; Indels 7; Gaps 6;
QY      3475  CTGTTAATACAGATTTCTCTCATATCTGATTTTCAGATTAATTAGAACACGCTTAGGAA 3534
Db      1  CTGTTAATACAGATTTCTCTCATATCTGATTTTCAGATTAATTAGAACACGCTTAGGAA 60
QY      3535  GTAGTCATGATCTCAGGTTTGTTCGAGACACCTGATGACCTTATGATGATGATGATG 3594
Db      61  GTAGTCATGATCTCAGGTTTGTTCGAGACACCTGATGACCTTATGATGATGATGATG 120
QY      3595  TAAAGGAAGTACTAGTTTGTGGAATAATGACATTAAGGAAGTCTGCTGTTTTTGA 3654
Db      121  TAAAGGAAGTACTAGTTTGTGGAATAATGACATTAAGGAAGTCTGCTGTTTTTGA 180
QY      3655  AAAGCGTCCAGAAAGAGAGCTTAGCAGAGAGTCTTACCCATACACATTTGG 3714
Db      181  AAAGCGTCCAGAGAGAGAGCTTAGCAGAGAGTCTTACCCATACACATTTGG 240
QY      3715  CTCAGGTTTCCAGAGAGGAGGCAAGAAATTAGAGTCTTCAAGAGAACTTATCTAGTG 3774
Db      241  CTCAGGTTTCCAGAGAGGAGGCAAGAAATTAGAGTCTTCAAGAGAACTTATCTAGTG 300
QY      3775  AGAGTAAGAGGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTT 3834
Db      301  AGAGTAAGAGGCTTCCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTT 359
QY      3835  CTCAGTCTACTAGCATTAGCAGCAGTCTTCCAGAGTCTCTGTCTAAGAACACAGAGAGA 3894
Db      360  CTCAGTCTACTAGCATTAGCAGCAGTCTTCCAGAGTCTCTGTCTAAGAACACAGAGAGA 419
QY      3895  ATTTATTTATATGAAGAATAGTCTTAATATGATCTGCAATACCAAGTATATTTGGCAAGG 3954
Db      420  ATTTATTTATATGAAGAATAGTCTTAATATGATCTGCAATACCAAGTATAT-TGGCAAGG 478

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Db      301 TGAACAAGAGGCTCTGAGACCTGCTCAGGCGTATCCCTCAGAGTGACATTTTAACAC 360
Qy      4301 TCAGCAGAGGATACCATGCAACATTAACCTGATTAAGCTCCAGAGAAATGGCTGACT 4360
Db      361 TCAGCAGAGGATACCATGCAACATTAACCTGATTAAGCTCCAGAGAAATGGCTGACT 420
Qy      4361 AGAGCTGTGTAAACAGCATGGAGCCAGCTTCAACAGCTACCTTCATCATTAAG 4420
Db      421 AGAGCTGTGTAAACAGCATGGAGCCAGCTTCAACAGCTACCTTCATCATTAAG 480
Qy      4421 TGACTCTTTCGCTTGAAGACCTGCAAAATCCAGAAACAAAGCAGATCAGAAAAGAGT 4480
Db      481 TGACTCTTTCGCTTGAAGACCTGCAAAATCCAGAAACAAAGCAGATCAGAAAAGAGT 540
Qy      4481 ATTAACTTCAAGAAAAGTGTGAATACCTATTAAGCCAGAAATCCAGAGGCTTTCTGC 4540
Db      541 ATTAACTTCAAGAAAAGTGTGAATACCTATTAAGCCAGAAATCCAGAGGCTTTCTGC 600
Qy      4541 TGACAAGTTGAGGTGTCTGAGATAGTTCTACAGATAAAATAAGACAGAGTGA 4600
Db      601 TGACAAGTTGAGGTGTCTGAGATAGTTCTACAGATAAAATAAGACAGAGTGA 660
Qy      4601 AAGGTCAATCCCTTCTTAATGCCCCATCATTAAGATAGTGTG 4643
Db      661 AANNCAT -CCCTTCTTAATGCCATCATTAAGATAGTGTG 702

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RESULT 11
Bg777447 747 bp mRNA linear EST 15-MAY-2001
LOCUS 602664758P1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4804551 5',

DEFINITION mRNA sequence.
Bg777447.1 GI:14047764

ACCESSION Bg777447
VERSION Bg777447.1
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 747)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov

Plate: LCM1651 row: c column: 16
High quality sequence stop: 725.

FEATURES
Location/Qualifiers

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1..747
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4804551"
/clone_id="NIH MGC 60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: prostate; Vector: pDR-LIB (Clontech);
Site_1: SfiI (ggcgccctgggc); Site_2: SfiI (ggcattatggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCAGCGCCGACATG-3' (30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech

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Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

BASE COUNT 232 a 160 c 162 g 193 t

ORIGIN

Query Match 12.0%; Score 687.6; DB 12; Length 747;
Best Local Similarity 97.7%; Pred. No. 2,9e-151;
Matches 729; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

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Qy      1 AGTCGCTGAGACTTCTTGAGCCCGACACCAGGCTGTGGGCTTCTCAGATAACTGGCC 60
Db      3 AGTCGCTGAGACTTCTTGAGCCCGACACCAGGCTGTGGGCTTCTCAGATAACTGGCC 61
Qy      61 CCTGGCCTCAGAGAGGCTTCAACCTGCTGCTGGGTAAGTTCATTTGAGCAAGAAAGAA 120
Db      62 CTTGGCCTCAGAGAGGCTTCAACCTGCTGCTGGGTAAGTTCATTTGAGCAAGAAAGAA 121
Qy      121 TGGATTATCTGCTCTTGGCTTGAAGATACAAATGTCAATTATGCTATGCAGAAA 180
Db      122 TGGATTATCTGCTCTTGGCTTGAAGATACAAATGTCAATTATGCTATGCAGAAA 181
Qy      181 TCTTAAGTGTCCCATCTGTCTGGAAGTTCAGAGAACCTGTCTCAGAAATGTGACC 240
Db      182 TCTTAAGTGTCCCATCTGTCTGGAAGTTCAGAGAACCTGTCTCAGAAATGTGACC 241
Qy      241 ACATATTTTGCAAAATTTTGATGCTGAAACCTTCAACCAAGAAAGAGGCTTCAAGT 300
Db      242 ACATATTTTGCAAAATTTTGATGCTGAAACCTTCAACCAAGAAAGAGGCTTCAAGT 301
Qy      301 GTCCCTTATGTAAGATATATATACCAAAAGAGGCTTCAAGAAAGTATGATTTAGTC 360
Db      302 GTCCCTTATGTAAGATATATATACCAAAAGAGGCTTCAAGAAAGTATGATTTAGTC 361
Qy      361 AACTTGTGAAGAGCTATTGAA -AATCATTTGTGCTTTTCAAGTTGACACAGGTTGGAG 419
Db      362 AACTTGTGAAGAGCTATTGAA -AATCATTTGTGCTTTTCAAGTTGACACAGGTTGGAG 421
Qy      420 TATGCAACAGCATATATTTTGCAAAAGAAATATACCTCTGCAACATCTTAAAGAT 479
Db      422 TATGCAACAGCATATATTTTGCAAAAGAAATATACCTCTGCAACATCTTAAAGAT 481
Qy      480 GAAGTTTCTATCATCCAAAGATATGAGGCTACAGAAACCGTGCCAAAGACTTTCAGAGT 539
Db      482 GAAGTTTCTATCATCCAAAGATATGAGGCTACAGAAACCGTGCCAAAGACTTTCAGAGT 541
Qy      540 GAAACCGAAATATCTTCTTTCAGAGAAACCAAGTCTAGTGTCAACTTCTTAACTTTGA 599
Db      542 GAAACCGAAATATCTTCTTTCAGAGAAACCAAGTCTAGTGTCAACTTCTTAACTTTGA 601
Qy      600 ACTGTGAGAACTCTGAGCAAAAGAGCGGATATCAACCTTCAAAAGAGCTGTCAATT 659
Db      602 ACTGTGAGAACTCTGAGCAAAAGAGCGGATATCAACCTTCAAAAGAGCTGTCTAACCTT 661
Qy      660 GAATGGAGTCTGATCTTCTGAAAGATACCGTTAATAGCAACTTATTTGCACTGT-GGG 718
Db      662 GAATGGAGTCTGATCTTCTGAAAGATACCGTTAATAGCAACTTATTTGCACTGT-GGG 721
Qy      719 AGATCAAGATTTGTACAAATCACCC 744
Db      722 AGATCAAGATTTGTACAAATCACCC 747

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RESULT 12

BF508987/c 739 bp mRNA linear EST 06-DEC-2000
LOCUS UI-H-B14-aac-b-06-0-UI.s1 NCI CGAP_Sub8 Homo sapiens cDNA clone
DEFINITION IMAGE:3085787 3', mRNA sequence.

ACCESSION BF508987
VERSION BF508987.1 GI:11592285

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at:
 http://image.llnl.gov
 Plate: LHM13341 row: 0 column: 21
 High quality sequence stop: 669.

FEATURES

source

Location/Qualifiers

1..878

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:606516"

/clone_1ib="NIH MGC 72"

/issue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: PCMV-SpOx; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 261 a 180 c 190 g 227 t
 ORIGIN

Query Match 12.4%; Score 706.2; DB 14; Length 878;
 Best Local Similarity 98.8%; Pred. No. 1.2e-155;

Matches 754; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

30 CAGGCTGGGGTTTCTCAGATTAAGGCCCCCTGGCTCAGAGGCTTACCTCTGCG 89
 13 CAGGCTGGGGTTTCTCAGATTAAGGCCCCCTGGCTCAGAGGCTTACCTCTGCG 72
 90 TCTGGGTAAGTTCATTTGGAACAGAAAGAAATGATTTATCTCTTGGCGTTGAAGA 149
 73 TCTGGGTAAGTTCATTTGGAACAGAAAGAAATGATTTATCTCTTGGCGTTGAAGA 132
 150 GTACAAAATGTCATTAATGCTATGAGAAATCTTGAAGTCCATCTGTCTGAGTTG 209
 133 GTACAAAATGTCATTAATGCTATGAGAAATCTTGAAGTCCATCTGTCTGAGTTG 192
 210 ATCAAGAACTGTCTCCACAAAGTGTGACCAATATTTTGCATTTGATGCTGAAA 269
 193 ATCAAGAACTGTCTCCACAAAGTGTGACCAATATTTTGCATTTGATGCTGAAA 252
 270 CTTCCACCCGAAAGAGGCGCTTACAGTGTCTTATTTGAAGATATATACCAA 329
 253 CTTCCACCCGAAAGAGGCGCTTACAGTGTCTTATTTGAAGATATATACCAA 312
 330 AGAGCCCTACAAAGAGTACGAGATTAGTCAACTGTGAGAGCTATTGAAAATCAT 389
 313 AGAGCCCTACAAAGAGTACGAGATTAGTCAACTGTGAGAGCTATTGAAAATCAT 372
 390 TGTGCTTTACGCTTGACACAGGTTTGAAGTATGCAACAGCTATATTTGCAAAAAG 449
 373 TGTGCTTTACGCTTGACACAGGTTTGAAGTATGCAACAGCTATATTTGCAAAAAG 432
 450 GAAATTAATCTCTCTGACATCTAAAGATGAAGTTTCTATCATCCAAAGTATGGCTAC 509
 433 GAAATTAATCTCTCTGACATCTAAAGATGAAGTTTCTATCATCCAAAGTATGGCTAC 492
 510 AGAAACCGTCCAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTTTCGAGAGAAC 569
 493 AGAAACCGTCCAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTTTCGAGAGAAC 549
 570 AGTCTCAGTGTCCAACTCTTAACCTTGAGACTGTGAGAACTCTGAGCAAAAGCAGCG 629
 550 AGTCTCAGTGTCCAACTCTTAACCTTGAGACTGTGAGAACTCTGAGCAAAAGCAGCG 609
 630 ATACAACTCAAAAGAGCTCTGTCTACATTTGAATGGAGTCTGATTTCTTGAAGATACC 689
 610 ATACAACTCAAAAGAGCTCTGTCTACATTTGAATGGAGTCTGATTTCTTGAAGATACC 669
 690 GTTATATAAGCACTTATTGAGT-GTGGAGATCAAGAAATGTTTAAATCAATCAATCAATCA 748
 670 GTTATATAAGCACTTATTGAGTGTGGAGATCAAGAAATGTTTAAATCAATCAATCAATCA 729
 749 AGGAACA-GGGATGAATCAG-TTGTGATCTGCAAAAAG 789

DB 730 AGGACCAAGGAGTGAATTCAGTTTGGATTCTGCACAAAAAG 772

RESULT 10
 LOCUS
 DEFINITION

AUI25312 AUI25312 702 bp mRNA linear EST 01-AUG-2002

ACCESSION AUI25312 NT2RM4 Homo sapiens CDNA clone NT2RM4001388 5', mRNA

VERSION AUI25312.1 GI:10950028

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 702)

REFERENCE Ota, T., Makamatsu, A., Ozawa, M., Ishii, S., Saio, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and

Isogai, T. HRI human CDNA project (Ota, T., Makamatsu, A., Ozawa, M., Ishii, S., Saio, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T.)

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3875

Fax: 81-438-52-3886

Email: genomics@hri.co.jp

HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; CDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES
 source

1..702
 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="NT2RM4001388"

/clone_1ib="NT2RM4"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"

BASE COUNT 235 a 142 c 163 g 159 t 3 others

ORIGIN

Query Match 12.0%; Score 688; DB 9; Length 702;
 Best Local Similarity 99.4%; Pred. No. 2.2e-151;

Matches 699; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

3941 AATATGGCAAGGATCTCAGAAACATCACCTTAGTGAAGAAACAAATGTTCTGTAG 4000
 1 AATATGGCAAGGATCTCAGAAACATCACCTTAGTGAAGAAACAAATGTTCTGTAG 60
 4001 CTGTTTCTTCCACAGTCACTGAATGGAAGCTTGAATGCAATCAATCAATCAATCA 4060
 61 CTGTTTCTTCCACAGTCACTGAATGGAAGCTTGAATGCAATCAATCAATCAATCA 120
 4061 TCCCTTCTTGAATGGTCTTCCAAACAAATGAGCATCAGTCTGAAAGCCAGGAGTTGG 4120
 121 TCCCTTCTTGAATGGTCTTCCAAACAAATGAGCATCAGTCTGAAAGCCAGGAGTTGG 180
 4121 TCTGAGTCAAGGAATGTTGTTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAA 4180
 181 TCTGAGTCAAGGAATGTTGTTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAA 240
 4181 TAAATCAAGGAAGCAATGATGATCAATCTTGAAGCAATGATGATGATGATGATGATG 4240
 241 TAAATCAAGGAAGCAATGATGATCAATCTTGAAGCAATGATGATGATGATGATGATG 300
 4241 TGAACAAGGCTCTCTGAGAGCTCTCAGAGGCTATCTCTCAGAGTACATTTTAAACAC 4300

Db 541 CTATTTCGGGTGACCCAGCTCTATTAAAGAAAGAAATCTGATGAGCATGATTTTGA 600
Qy 5324 AGTCAGAGAGATGTGTCATATGAGAGAAACCAACCAAGTCCAAAGCAGCAAGATC 5383
Db 601 AGTCAGAGAGATGTGTCATATGAGAGAAAGCAACCAAGTCCAAAGCAGCAAGATC 660
Qy 5384 CCAGAGAGAGAAATCTTCAGGGGGGCTAGAAATCTGTGCTATGAGGCGCTTCCCAACAT 5443
Db 661 CCAGAGAGAGAAATCTTCAGGGGGGCTAGAAATCTGTGCTATGAGGCGCTTCCCAACAT 720
Qy 5444 GCCCAGATCACTGGAATG 5465
Db 721 GCCCAGATCACTGGAATG 742

RESULT 8
BQ422380 899 bp mRNA linear EST 23-MAY-2002
LOCUS AGENCOURT 7802085 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042052
DEFINITION 5', mRNA sequence.
ACCESSION BQ422380.1 GI:21117695
VERSION BQ422380
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 899)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13280 row: n column: 05
High quality sequence stop: 597.
Location/Qualifiers
1..899
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6042052"
/clone_id="NIH_MGC_92"
/tissue="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

BASE COUNT 291 a 182 c 192 g 230 t 4 others
ORIGIN

Query Match 12.9%; Score 734.6; DB 14; Length 899;
Best Local Similarity 97.1%; Pred. No. 2,4e-162;
Matches 824; Conservative 0; Mismatches 11; Indels 14; Gaps 7;

Qy 30 CAGCGTGTGGGGTTTCACAGTAACCTGCGCCCTCGCTCGAGAGGCTTACCTCTGC 89
Db 16 CAGCGTGTGGGGTTTCACAGTAACCTGCGCCCTCGCTCGAGAGGCTTACCTCTGC 75
Qy 90 TCTGGTAAAGTTCATTTGAGACAGAAAGAAATGATTATGCTTGGCTTGAAGAA 149
Db 76 TCTG-----GTTCTTGAACAGAAAGAAATGATTATGCTTGGCTTGAAGAA 129
Qy 150 GTACAAATGTCATTAATGCTATGACAGAAATCTTGAATGCTCCATCTGCTGAGATTG 209

Db 130 GTACAAATGTCATTAATGCTATGACAGAAATCTTGAATGCTCCATCTGCTGAGATTG 189
Qy 210 ATCAAGAACTCTCTCCCAAGAGTGTACCAACATATTTTGAATTTGACATGCTGAA 269
Db 190 ATCAAGAACTCTCTCCCAAGAGTGTACCAACATATTTTGAATTTGACATGCTGAA 249
Qy 270 CTCTCAACAGAGAAAGGCGCTTACAGTGTCTTTATGTAAATGATATATACCA 329
Db 250 CTCTCAACAGAGAAAGGCGCTTACAGTGTCTTTATGTAAATGATATATACCA 309
Qy 330 AGAGCTTCAAGAGAAATGACAGATTAGTCAACTTTGTAAGAGCTATTAATATCATT 389
Db 310 AGAGCTTCAAGAGAAATGACAGATTAGTCAACTTTGTAAGAGCTATTAATATCATT 369
Qy 390 TGTGCTTTTCAAGTGTACAGAGTTGGAGTATGCAACGCTATATTTTGAAGAAAG 449
Db 370 TGTGCTTTTCAAGTGTACAGAGTTGGAGTATGCAACGCTATATTTTGAAGAAAG 429
Qy 450 GAAATTAACCTCTCTGACATCTTAAAGATGAAATTTCTATATCCAAAGTATGGCTAC 509
Db 430 GAAATTAACCTCTCTGACATCTTAAAGATGAAATTTCTATATCCAAAGTATGGCTAC 489
Qy 510 AGAACCCTGTCACAAAGACTTCTACAGAGTGAACCCGAAATCTTCTGACAGAAAC 569
Db 490 AGAACCCTGTCACAAAGACTTCTACAGAGTGAACCCGAAATCTTCTGACAGAAAC 546
Qy 570 AGTCTAGTGTCCAACTCTCTTACCTTGAACCTGTAGAACTGTAGGACAAAGCGCG 629
Db 547 AGTCTAGTGTCCAACTCTCTTACCTTGAACCTGTAGAACTGTAGGACAAAGCGCG 606
Qy 630 ATCAACCTTCAAGAGAGCTGTCTACATTTGAGATTTGATTTCTGAGAGATAC 689
Db 607 ATCAACCTTCAAGAGAGCTGTCTACATTTGAGATTTGATTTCTGAGAGATAC 666
Qy 690 GTTAATTAAGGCACTTATGACAGTGTGGAGATCAAGATTTTCAATCACCCTCAA 749
Db 667 GTTAATTAAGGCACTTATGACAGTGTGGAGATCAAGATTTTCAATCACCCTCAA 726
Qy 750 GGAACCA-GGAGATGAAATGCTTTGATTTCTGAAAAAGGCTGC-TTGGAATTTTCTG 807
Db 727 GGAACCAAGGAGATGAAATGCTTTGATTTCTGAAAAAGGCTTTGGAATTTTCTG 786
Qy 808 AGACGATGTAAACA-ATACTGAACATC-ATCAACCCAGTAATATGA-TTTGACACCA 864
Db 787 AGACGATGTGTAAACAATCTGAATCATCATCAACCGTAATATGATTTTGAACCA 846
Qy 865 CTGAGAAAC 873
Db 847 CTGAGAAAC 855

RESULT 9
BQ215100 878 bp mRNA linear EST 02-MAY-2002
LOCUS AGENCOURT 7591049 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:605516
DEFINITION 5', mRNA sequence.
ACCESSION BQ215100.1 GI:20396500
VERSION BQ215100
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Query Match 13.3%; Score 761.8; DB 9; Length 783;
Best Local Similarity 99.2%; Pred. No. 8.8e-169;
Matches 774; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

BASE COUNT 255 a 146 c 185 g 194 t 3 others
ORIGIN

Query Match 13.3%; Score 761.8; DB 9; Length 783;
Best Local Similarity 99.2%; Pred. No. 8.8e-169;
Matches 774; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

3579 TTAGATGATGGAATTAAGAGAGTACTAGTTTGTGGAATAATGACATTAAGAGAACT 3638
1 TTAGATGATGGAATTAAGAGAGTACTAGTTTGTGGAATAATGACATTAAGAGAACT 60
3639 TCTGCTGTTTTCAGCAAGCGTCCAGAAAGAGAGAGTCTAGAGAGTCTTCTTTC 3698
61 TCTGCTGTTTTCAGCAAGCGTCCAGAAAGAGAGAGTCTAGAGAGTCTTCTTTC 120
3699 ACCCTTACACATTTGGCTCAGGTTACCGAAGAGGCGCAAGAAATTAGAGTCTAGAA 3758
121 ACCCTTACACATTTGGCTCAGGTTACCGAAGAGGCGCAAGAAATTAGAGTCTAGAA 180
3759 GAGAACTTATCTAGTGAAGTGAAGAGTCTTCCCTGCTCCACACTGTTATTTGTTAA 3818
181 GAGAACTTATCTAGTGAAGTGAAGAGTCTTCCCTGCTCCACACTGTTATTTGTTAA 240
3819 GTAAACAATATCTCTTCTCAGTCTACTAGAGATAGACCGTGTCTACCGAGTCTGTCT 3878
241 GTAAACAATATCTCTTCTCAGTCTACTAGAGATAGACCGTGTCTACCGAGTCTGTCT 300
3879 AAGAACACAGAGAGAGATTTATTCATTTGAAGATAGCTTAAATGATGCTGACGTAACG 3938
301 AAGAACACAGAGAGAGATTTATTCATTTGAAGATAGCTTAAATGATGCTGACGTAACG 360
3939 GTAAATTTGGCAAGAGATCTCAGAGACATCACTTATGAGAGAAACAAATGTTCTGT 3998
361 GTAAATTTGGCAAGAGATCTCAGAGACATCACTTATGAGAGAAACAAATGTTCTGT 420
3999 AGCTTGTCTTCTTCAAGTCAAGTGAATTTGAAGATTTGACCTCAATTAACAACCCAG 4058
421 AGCTTGTCTTCTTCAAGTCAAGTGAATTTGAAGATTTGACCTCAATTAACAACCCAG 480
4059 GATCTTCTTCTTCAAGTCAAGTGAATTTGAAGATTTGACCTCAATTAACAACCCAG 4118
481 GATCTTCTTCTTCAAGTCAAGTGAATTTGAAGATTTGACCTCAATTAACAACCCAG 540
4119 GGTGAGTGAACAAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAGAG 4178
541 GGTGAGTGAACAAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAGAG 600
4179 AATATCAAGAGAGAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAG 4238
601 AATATCAAGAGAGAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAG 660
4239 AGTGAACAAGAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAGAG 4297
661 AGTGAACAAGAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAGAG 720
4298 CACTCAGAGAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAGAGAG 4357
721 CACTCAGAGAGAGATTTGTTTCAAGTGAATTTGAAGAGAGAGAGAGAGAGAGAGAG 780

RESULT 7
BG681276 743 bp mRNA linear EST 01-MAY-2001
LOCUS 602627125F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:475187 5',
DEFINITION mRNA sequence.
ACCESSION BG681276
VERSION BG681276.1 GI:13912673
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 743)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10609 row: a column: 08
High quality sequence stop: 741.

FEATURES
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 233 a 156 c 182 g 172 t
ORIGIN

Query Match 13.0%; Score 740.4; DB 12; Length 743;
Best Local Similarity 99.9%; Pred. No. 9.7e-164;
Matches 741; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4724 GGAGCAACAGCTGGAAGAGTGTGGGCCACAGATTTGACGGAACATCTTACCTTCCAG 4783
1 GGAGCAACAGCTGGAAGAGTGTGGGCCACAGATTTGACGGAACATCTTACCTTCCAG 60
4784 GCAAGATTTAAGGGAACCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACC 4843
61 GCAAGATTTAAGGGAACCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACC 120
4844 TGAATCTGATCTTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4903
121 TGAATCTGATCTTCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
4904 TTCAACCTCTGATTTGAAAGTTCCCAATTGAAAGTTGCAAGATCTGCGAGATCCAGC 4963
181 TTCAACCTCTGATTTGAAAGTTCCCAATTGAAAGTTGCAAGATCTGCGAGATCCAGC 240
4964 TGTGCTCATATCTGATATCTGTTGGTATTAATGCAATGGAAGAGAGAGAGAGAGAG 5023
241 TGTGCTCATATCTGATATCTGTTGGTATTAATGCAATGGAAGAGAGAGAGAGAGAG 300
5024 GAAGCGAATTTGACAGCTTCAACAGAAAGGTCACAAAGATGTCATGAGTGTGTC 5083
301 GAAGCGAATTTGACAGCTTCAACAGAAAGGTCACAAAGATGTCATGAGTGTGTC 360
5084 TGGCTTGAACCCAGAGAAATTTATCTGTTCAAGATTTGCGAGAAACACCAATCAGC 5143
361 TGGCTTGAACCCAGAGAAATTTATGCTCGTTCAAGATTTGCGAGAAACACCAATCAGC 420
5144 TTAACTAATTAATTTCTGAGAGATCTCATGTTGTTATGAAACAGATCTGAGTT 5203
421 TTAACTAATTAATTTCTGAGAGATCTCATGTTGTTATGAAACAGATCTGAGTT 480
5204 TGTGTTGAACCGGACACTGAATATTTCTAGAGATTGGCGGAGGAAATGGTACTTTG 5263
481 TGTGTTGAACCGGACACTGAATATTTCTAGAGATTGGCGGAGGAAATGGTACTTTG 540
5264 CTATTTCTGGGTGACCCAGTCTATTTAAGAGAAAGAAATGCTGAATGAGCATGATTTGA 5323

QY 2879 ACAGACA 2885
 Db 971 AACGAAA 977

RESULT 5
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 LOCUS
 DEFINITION AUI22476 MAMMAL Homo sapiens cDNA clone MAMMA1002447 5', mRNA
 sequence.
 AUI22476
 ACCESSION
 VERSION AUI22476.1 GI:10937746
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 845)
 Oca.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
 Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
 Isogai.T.
 HRI human cDNA project
 Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1..845
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 /clone_lib="MAMMA1"
 /tissue_type="mammary gland"
 /note="Vector: pME18SFL3"

BASE COUNT 279 a 172 c 191 g 200 t 3 others

ORIGIN

Query Match 14.2%; Score 811.8; DB 9; Length 845;
 Best Local Similarity 99.1%; Pred. No. 1.4e-180;
 Matches 836; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 3819 GTAAACAATACCTTCTCAGTCTACAGATGACACCGTGTCTACCGAGTCTCTCT 3878
 Db 1 GTAAACAATATACCTTCTCAGTCTACAGATGACACCGTGTCTACCGAGTCTCTCT 60

QY 3879 AAGAACAAGAGAGATTTATTTATTCATTGAGAAATAGCTTAATGACTGAGTAACAG 3938
 Db 61 AAGAACAAGAGAGATTTATTTATTCATTGAGAAATAGCTTAATGACTGAGTAACAG 120

QY 3939 GTAATATTTGCAAGAGATCTCAGAAATCATCCTTAGTGTAGAGAAACAAATGTTCTGCT 3998
 Db 121 GTAATATTTGCAAGAGATCTCAGAAATCATCCTTAGTGTAGAGAAACAAATGTTCTGCT 180

QY 3999 AGCTGTCTTCTTACAGTGTAGAGATTTGGAAGTGTGACTGCAATATACAAACACCG 4058
 Db 181 AGCTGTCTTCTTACAGTGTAGAGATTTGGAAGTGTGACTGCAATATACAAACACCG 240

QY 4059 GATCCTTCTTGTGTTGTTCTTCCAAACAATGAGGATCAGTCTGAAAGCCAGGAGTT 4118
 Db 241 GATCCTTCTTGTGTTGTTCTTCCAAACAATGAGGATCAGTCTGAAAGCCAGGAGTT 300

QY 4119 GGTCTGAGTGAAGAAGATTTGTTTCAAGATGATGAAGAAAGAGACGGCTTGAAGAA 4178
 Db 301 GGTCTGAGTGAAGAAGATTTGTTTCAAGATGATGAAGAAAGAGACGGCTTGAAGAA 360

QY 4179 AATAATCAAGAAAGAGCAATGATTCCTTAACTTAGTGAAGACAGATCTGGTGTGAG 4238
 Db 361 AATAATCAAGAAAGAGCAATGATTCCTTAACTTAGTGAAGACAGATCTGGTGTGAG 420

QY 4239 AGTGAACAAGCGCTCTCTGAGAGCTGCTCAGGGCTATCTCTTCTGAGTGAATTTTACC 4298
 Db 421 AGTGAACAAGCGCTCTCTGAGAGCTGCTCAGGGCTATCTCTTCTGAGTGAATTTTACC 480

QY 4299 ACTCAGACAGAGGATATCCATGCAACTTAACCTGATTAAGTCCAGAGGAAATGGCTGAA 4358
 Db 481 ACTCAGACAGAGGATATCCATGCAACTTAACCTGATTAAGTCCAGAGGAAATGGCTGAA 540

QY 4359 CTAGAAGCTGTGTTAGAACAGCATGGAGAGCAGCTTCTTAAAGCTTACCTTCATCAT 4418
 Db 541 CTAGAAGCTGTGTTAGAACAGCATGGAGAGCAGCTTCTTAAAGCTTACCTTCATCAT 600

QY 4419 AGTGAAGCTGTGTTAGAACAGCATGGAGAGCAGCTTCTTAAAGCTTACCTTCATCAT 4478
 Db 601 AGTGAAGCTGTGTTAGAACAGCATGGAGAGCAGCTTCTTAAAGCTTACCTTCATCAT 660

QY 4479 GTATTAACTTCAAGAAAGATAGTGAATACCTTAAAGCTTAAAGCTTAAAGCTTAA 4538
 Db 661 GTATTAACTTCAAGAAAGATAGTGAATACCTTAAAGCTTAAAGCTTAAAGCTTAA 720

QY 4539 GCTGACAGATTTGAGGTGTGAGATAGTGTACAGATTTAAATTAAGAACACAGGA -G 4596
 Db 721 GCTGACAGATTTGAGGTGTGAGATAGTGTACAGATTTAAATTAAGAACACAGGA 780

QY 4597 TGAAGAGGTCA-TCCCTCTTAAATGCCATCTTATGATGATGATGATGATGATGATG 4655
 Db 781 TGAAGAGGTCA-TCCCTCTTAAATGCCATCTTATGATGATGATGATGATGATGATGATG 840

QY 4656 TGCT 4659
 Db 841 TGCT 844

RESULT 6
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 LOCUS
 DEFINITION AUI42729 Y79AA1 Homo sapiens cDNA clone Y79AA1000792 5', mRNA
 sequence.
 AUI42729
 ACCESSION
 VERSION AUI42729.1 GI:11004250
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 783)
 Oca.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
 Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
 Isogai.T.
 HRI human cDNA project
 Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1..783
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 /db_xref="taxon:9606"
 /clone="Y79AA1000792"
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 QY 4931 ATTGAAGTTGAGATCTGCCAGTCCAGTCTGCTCAATCAATCAATCTGCTG 4990
 Db 495 ATTGAAGTTGAGATCTGCCAGTCCAGTCTGCTCAATCAATCAATCTGCTG 554
 QY 4991 GTATATGCAATGAGAAAGTGTGAGCAGAGGAGAAAGCAATGAGCTTCAACAG 5050
 Db 555 TTATATGCAATGAGAAAGTGTGAGCAGAGGAGAAAGCAATGAGCTTCAACAG 614
 QY 5051 AAGGTCACCAAAAGATCTCAATGCTGTCTGCTGAGCCCAAGAAATTTATGCT 5110
 Db 615 AAGGTCACCAAAAGATCTCAATGCTGTCTGCTGAGCCCAAGAAATTTATGCT 674
 QY 5111 CGTGTACAAAGTTTGCAGAAACACCACTCACTTAACTAATCAATCAATCAATGAG 5170
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 Db 735 TACTCATGTTTGTATGAAACAGATCTGATGTTGTGTGAAACGACACTGAATATTT 794
 QY 5231 TCTAGCAATTCGCGGAGAGAAATGGGTAGTTCATATTTCTGGGTGACCCAGTCTATTA 5290
 Db 795 TCTAGCAATTCGCGGAGAGAAATGGGTAGTTCATATTTCTGGGTGACCCAGTCTATTA 854
 QY 5291 AGAAGAAATATGCTGATGAGCATGATTTTGAAGTCAGAGAGATGGT--TCAATGGA 5348
 Db 855 AGAAGAAATATGCTGATGAGCATGATTTTGAAGTCAGAGAGATGGTCTCAATGGA 914
 QY 5349 AGAAGCAACCAAGTCCAAAGCGAG 5373
 Db 915 AGAAGCAACCAAGTCCAAAGCGAG 939
 RESULT 4
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 LOCUS AGENCOURT_6386302 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5526666
 DEFINITION 5', mRNA sequence.
 ACCESSION BM452288
 VERSION BM452288.1 GI:18501328
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1089)
 NIH-MGC http://mgi.mc.nhl.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M12200 row: k column: 19
 High quality sequence stop: 667.
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 Source location/Qualifiers
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BASE COUNT 389 a 212 c 248 g 240 t
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 Best Local Similarity 96.2%; Pred. No. 2.8e-188;
 Matches 930; Conservative 0; Mismatches 29; Indels 8; Gaps 6;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies.
 QY 1925 TTCAAAAGACCTAAAGAAATAGGCTGAGAGAGAGCTTCTACAGCATATTCATGC 1984
 Db 13 TTCAAAAGACCTAAAGAAATAGGCTGAGAGAGAGCTTCTACAGCATATTCATGC 72
 QY 1985 GCTTGAACCTAGTACAGTAAATCTAAGCCCACTAATGTAATGCAATTTGA 2044
 Db 73 GCTTGAACCTAGTACAGTAAATCTAAGCCCACTAATGTAATGCAATTTGA 132
 QY 2045 TAGTGTCTTACAGTGAAGATTAAGAAAAAAGTACCAACCAATGCGAGGCA 2104
 Db 133 TAGTGTCTTACAGTGAAGATTAAGAAAAAAGTACCAACCAATGCGAGGCA 192
 QY 2105 CAGCAGAAACCTCAACATCAGAAAGTAAAGAACTGCACTGAGCCAGAGATTA 2164
 Db 193 CAGCAGAAACCTCAACATCAGAAAGTAAAGAACTGCACTGAGCCAGAGATTA 252
 QY 2165 CAGCAGAAATGAACAGACAAATGAAGACATGACAGCATCTTCCAGAGCTGAAGTT 2224
 Db 253 CAGCAGAAATGAACAGACAAATGAAGACATGACAGCATCTTCCAGAGCTGAAGTT 312
 QY 2225 AACAAATGACCTGCTTTTCTTACTAAGTTCAAATACAGTGAACCTTAAAGATTTGT 2284
 Db 313 AACAAATGACCTGCTTTTCTTACTAAGTTCAAATACAGTGAACCTTAAAGATTTGT 372
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 Db 373 CAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTAATAACGTAAAGTCTTA 432
 QY 2345 TAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAACTGAAG 2404
 Db 433 TAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAACTGAAG 492
 QY 2405 ATCTGTAGAGATGACAGTATTTCACTGTTAAGTGAAGAGGTTTGGCAACTGAAG 2464
 Db 493 ATCTGTAGAGATGACAGTATTTCACTGTTAAGTGAAGAGGTTTGGCAACTGAAG 552
 QY 2465 TATCTGCTTACGGAAGTTAGCACTCTTAGGAAGCAAAAACAGAACCAATTAATGTGT 2524
 Db 553 TATCTGCTTACGGAAGTTAGCACTCTTAGGAAGCAAAAACAGAACCAATTAATGTGT 612
 QY 2525 GAGTCAGTGTGACGATTTGAAGACCCCAAGGACTAATTCATGTTGTTCCAAAGTAA 2584
 Db 613 GAGTCAGTGTGACGATTTGAAGACCCCAAGGACTAATTCATGTTGTTCCAAAGTAA 672
 QY 2585 TAGAATGACACAGAGGCTTTAATATCACTTGGACATGAAGTTAACCACTGCGGA 2644
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 QY 2645 AACAGCATGAAT--GGAAGAAAGTGAAGTGTGCTCAATTTGGCAATATCAATTA 2703
 Db 733 AACAGCATGAAT--GGAAGAAAGTGAAGTGTGCTCAATTTGGCAATATCAATTA 792
 QY 2704 AGGTTTCAAGAGGCGAGCATTTGCTGCTGTTTCAAAATCCAGAAATGCGAAGAGGAAT 2763
 Db 793 A-GTTTCAAGAGGCGAGCATTTGCTGCTGTTTCAAAATCC-GGAAGAAAGCAAGAGAT 850
 QY 2764 GTGCAACATCTCTGCCCACCTCTGGGTCC-TTAAAGAAACAAAGTCCAAAGTCACTTTT 2822
 Db 851 GTGCAACATCTCTGCCCACCTCTGGGTCC-TTAAAGAAACAAAGTCCAAAGTCACTTTT 910
 QY 2823 GAATGTGAACAAA--GGAAGAAATCAAGAAAGATGATTA-TATCAAGCTGT 2878
 Db 911 GAATGTGAACAAA--GGAAGAAATCAAGAAAGATGATTA-TATCAAGCTGT 970


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Db      1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAAAGATGGAATTAAGCAGAACTGCCATGCT 1200
Qy      1201 CAGAGAACTCTAGAGATGAGATGAGATGCTCTGGATTAACCTAATATAGAGAGATTCAGA 1260
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Qy      1261 AAGTTAATGAGTGTCTTCAGAAAGTATGATGAGTGTGATGATGATGATGATGATGATGATG 1320
Db      1261 AAGTTAATGAGTGTCTTCAGAAAGTATGATGAGTGTGATGATGATGATGATGATGATGATG 1320
Qy      1321 GGGAGTCTGATCAATCAATGCCAAAGTATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db      1321 GGGAGTCTGATCAATCAATGCCAAAGTATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy      1381 AATATCTGCTGCTTCAGAGAAAAATAGACTTACCTGAGCAGATGATGATGATGATGATGATGAT 1440
Db      1381 AATATCTGCTGCTTCAGAGAAAAATAGACTTACCTGAGCAGATGATGATGATGATGATGATGAT 1440
Qy      1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGATTAATTTGAAGACAAATAT 1500
Db      1441 TATGTAAAGTGAAGAGTTCACCTCAATCAGTAGAGATTAATTTGAAGACAAATAT 1500
Qy      1501 TTGGGAAAAACCTTATCGGAAAGGCAAGCTCCCACTTAAAGCATGATGATGATGATGATGATGAT 1560
Db      1501 TTGGGAAAAACCTTATCGGAAAGGCAAGCTCCCACTTAAAGCATGATGATGATGATGATGATGAT 1560
Qy      1561 TAAATTATAGAGACATTTGTTACTAGGACACAGATTAATACAAAGAGCGTCCCTCAACATA 1620
Db      1561 TAAATTATAGAGACATTTGTTACTAGGACACAGATTAATACAAAGAGCGTCCCTCAACATA 1620
Qy      1621 AATTAAGCGTAAAGAGACCTACATCAGGCGCTTCACTCTGAGATTTTATCAAGAAAG 1680
Db      1621 AATTAAGCGTAAAGAGACCTACATCAGGCGCTTCACTCTGAGATTTTATCAAGAAAG 1680
Qy      1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATTAATTCAGGAACTTAACCAACGAGAGC 1740
Db      1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATTAATTCAGGAACTTAACCAACGAGAGC 1740
Qy      1741 AGAATGCTCAAGTATGATTAATTAATTAATGCTGATGATGATGATGATGATGATGATGATGAT 1800
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Qy      1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTGCTTCA 1860
Db      1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTGCTTCA 1860
Qy      1861 AAACGAAAGCTGAACCTTAATAGCAGATTAAGCAATATGGAATCTGAAATTAATATTC 1920
Db      1861 AAACGAAAGCTGAACCTTAATAGCAGATTAAGCAATATGGAATCTGAAATTAATATTC 1920
Qy      1921 ACAATTCAGAAAGCCTTAATAGAGTGGCTGAGAGAGAGTCTTCTTACAGAGGATATTC 1980
Db      1921 ACAATTCAGAAAGCCTTAATAGAGTGGCTGAGAGAGAGTCTTCTTACAGAGGATATTC 1980
Qy      1981 ATGGCTTGAACCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Db      1981 ATGGCTTGAACCTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
Qy      2041 TTGATAGTGTCTTCTAGCAGTGAAGATTAAGAAAAAGAAAGTATCAACCA 2090
Db      2041 TTGATAGTGTCTTCTAGCAGTGAAGATTAAGAAAAAGAAAGTATCAACCA 2090

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RESULT 3
LOCUS   B0068830
DEFINITION AGENCOURT 6740238 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802685
5', mRNA sequence.
ACCESSION B0068830

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VERSION B0068830.1 GI:19897888
EST
KEYWORDS
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 962)
          NIH-MGC http://mgs.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          plate: L1CM2037 row: h column: 14
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              /lab_host="DH10B (phage-resistant)"
              /note="Organ: Brain; Vector: pORF7; Site: 1: XhoI; Site: 2:
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              adaptor: GGCAAGG(C). Size-selected >500bp for average
              insert size 1.8kb. Library constructed by Ling Hong in
              the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-CDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

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FEATURES

source

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BASE COUNT 302 a 195 c 235 g 229 t 1 others
ORIGIN
Query Match 15.1%; Score 861.4; DB 14; Length 962;
Best Local Similarity 96.2%; Pred. No. 2.9e-192;
Matches 890; Conservative 0; Mismatches 33; Indels 2; Gaps 1;

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Db      255 TCAAGAGAGCTCATTAAGGTGTTGATGATGAGAGCAACAGCTGGAAGAGTGTGGGCC 314
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QY 1981 ATGGCGTTGAAGCTAGTACAGTAAATCTAAGCCACCTAATGTACTGAATGCAAA 2040
DB 1985 ATGGCGTTGAAGCTAGTACAGTAAATCTAAGCCACCTAATGTACTGAATGCAAA 2044
QY 2041 TTGATAGTGTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAA 2091
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BC030969 2090 bp mRNA linear HTC 13-JUN-2002
LOCUS Homo sapiens, similar to breast cancer 1, early onset, clone
DEFINITION IMAGE:4804551, mRNA.
ACCESSION BC030969
VERSION BC030969.1 GI:21411299
KEYWORDS HTC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2090)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mdickson@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
FEATURES
Source
1. 2090
Location/Qualifiers
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/lab_host="DH10B"
/note="Vector: pDNR-LIB"
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Best Local Similarity 99.3%; Pred. No. 0; Mismatches 14; Gaps 1;
Matches 2075; Conservative 0; Indels 1;
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DB 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTATATGCTATGCAAGAAA 180
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DB 181 TCTTGAAGTGTCCCATCTGCTGAGAGTGAATCAAGAACTGTCTCCACAAAGTGTACC 240
QY 241 ACATATTTTGGCAATTGTTGCAATGCTGAATCAATCTTCAACAGAGAAAGGGCTTTCACAGT 300
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DB 841 CCAGTAATATGATTTGAACACCACTGAGAGAGCTGAGCTGAGAGGATCCAGAAAGT 900
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLINL at: <http://image.llnl.gov>
Series: IRAL Plate: 19 Row: a Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA 91: 6552298
This clone has the following problem: incomplete processing.

FEATURES

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1. 2101

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/clone="IMAGE:399658"

/issue_type="Bladder, carcinoma"

/clone_id="NIH MGC_53"

/lab_host="DH10B"

/note="Vector: pDNr-LIB"

BASE COUNT 756 a 385 c 452 g 508 t

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Query Match 36.1% Score 2061.4; DB 11; Length 2101;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2079; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:46:15 ; Search time 6805 Seconds
(without alignments)
13591.833 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: em_estcua: *
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17: gb_gss: *
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27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2055.6	36.0	2090 11	BC030969 Homo sapi
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4	844.6	14.8	1089 13	BM452288 AGENCOURT
5	811.8	14.2	845 9	AU122476
6	761.8	13.3	783 9	AU142729

7	740.4	13.0	743 12	BG681276
8	734.6	12.9	899 14	BQ422380
9	706.2	12.4	878 14	BQ215100
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13	686.4	12.0	987 14	BM800251
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16	639	11.2	675 9	AL704228
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18	603.8	10.6	630 9	AT992240
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35	491.8	8.6	523 9	AA702344
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ALIGNMENTS

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ACCESSION BC012577
VERSION BC012577.1 GI:15214876
KEYWORDS
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ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LMU)
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan

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 Db 5101 AATTATGCTCGGTCAAGTGTGCAAGAAACACCAATCACTTAATCTAATTA 5160
 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAGAGAGAGAGAG 5220
 Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAGAGAGAGAGAG 5220
 QY 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280
 Db 5221 TGAATATTTTCTAGGAATGCGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280
 QY 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTGAAGTCAAGAGAGATGAG 5340
 Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAGATGATTTGAAGTCAAGAGAGATGAG 5340
 QY 5341 TCAATGGAAGAAACCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCT 5400
 Db 5341 TCAATGGAAGAAACCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCT 5400
 QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTTCACCAATGCTCCACAGATCAACTG 5460
 Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTTCACCAATGCTCCACAGATCAACTG 5460
 QY 5461 AATGATGATGAG 5520
 Db 5461 AATGATGATGAG 5520
 QY 5521 GCAAGAGTGTCAACCAATGTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
 Db 5521 GCAAGAGTGTCAACCAATGTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
 QY 5581 TCCATGCAATTTGGGAGAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
 Db 5581 TCCATGCAATTTGGGAGAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640

QY 5641 GTGTAGCACTTACAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
 Db 5641 GTGTAGCACTTACAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
 QY 5701 GCCACTACTGA 5711
 Db 5701 GCCACTACTGA 5711

Search completed: June 13, 2003, 00:36:31
 Job time : 1122 secs

Db	2341	CTAATATATCTGAAGACCCCAAGATCTCATGTAAAGTGAAGAAAGGTTTGCAACTG	2400
Qy	2401	AAAGATCTGTAGAGTAGACAGTAAATTTCAATGTGACTGTGTACTGATTAATGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGTAGACAGTAAATTTCAATGTGACTGTGTACTGATTAATGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAAGTTAGCACTTGGGAGGCCAAAAACAGACCAATTAAT	2520
Db	2461	AAAGTATCTGTTACTGGAAGTTAGCACTTGGGAGGCCAAAAACAGACCAATTAAT	2520
Qy	2521	GGTGTAGTACGTGTGAGCATTTTGAAACCCCAAGGACCTAATTCATGGTTGTTCCAAG	2580
Db	2521	GGTGTAGTACGTGTGAGCATTTTGAAACCCCAAGGACCTAATTCATGGTTGTTCCAAG	2580
Qy	2581	ATAATAGAAATACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACAACATC	2640
Db	2581	ATAATAGAAATACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACAACATC	2640
Qy	2641	GGGAAACAAGCATAGAAATGAGAAGAGTGAACCTTAGTCTCAGTATTTGCAGAAATACAT	2700
Db	2641	GGGAAACAAGCATAGAAATGAGAAGAGTGAACCTTAGTCTCAGTATTTGCAGAAATACAT	2700
Qy	2701	TCAAGTTTCAAAAGGCCAGTCAATTTGCTCTGTCTTTTCAATTCAGAAATGCAGAAAGG	2760
Db	2701	TCAAGTTTCAAAAGGCCAGTCAATTTGCTCTGTCTTTTCAATTCAGAAATGCAGAAAGG	2760
Qy	2761	AATGTGCACAATTCCTCTGCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAGATCACTT	2820
Db	2761	AATGTGCACAATTCCTCTGCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAGATCACTT	2820
Qy	2821	TTGAATGTGACAAAAGAAAGAAATCAAGAAAGATGACTTAATATCAAGCCTGAC	2880
Db	2821	TTGAATGTGACAAAAGAAAGAAATCAAGAAAGATGACTTAATATCAAGCCTGAC	2880
Qy	2881	AGACATTTAATATCACTGAGGCTTTCTGTGTGTGGTGCAGAAATATAGCCAGTTGATA	2940
Db	2881	AGACATTTAATATCACTGAGGCTTTCTGTGTGTGGTGCAGAAATATAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAGAGAGGCTCAGGTTTTGTCTATCATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAGAGAGGCTCAGGTTTTGTCTATCATCTCAGTTCAAGAGCA	3000
Qy	3001	ACGAATCTGCACTTACTCCAAATPAAACATGGAATTTTCAAAACCCATATGCTATAC	3060
Db	3001	ACGAATCTGCACTTACTCCAAATPAAACATGGAATTTTCAAAACCCATATGCTATAC	3060
Qy	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAGAAAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAATGTAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAACTTTGAGGAACATTCATAGTCACTGAAAGGAAATGGGAATAGAAACATTCOA	3180
Db	3121	AAACTTTGAGGAACATTCATAGTCACTGAAAGGAAATGGGAATAGAAACATTCOA	3180
Qy	3181	GTACAGTGCACAATTAGCCGTAATPACATTAAGAGAAATGTTTTTAAAGACGACGT	3240
Db	3181	GTACAGTGCACAATTAGCCGTAATPACATTAAGAGAAATGTTTTTAAAGACGACGT	3240
Qy	3241	CAAGCAATTTAATGAAGTAGGTTCAAGTACTAATGAAGTGCGCTCCAGTATTAATGAA	3300
Db	3241	CAAGCAATTTAATGAAGTAGGTTCAAGTACTAATGAAGTGCGCTCCAGTATTAATGAA	3300
Qy	3301	TAGGTTCCAGTATGAAAAATTCAGACGAACTAGGTGTAAGAAACGAGAGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAAAATTCAGACGAACTAGGTGTAAGAAACGAGAGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTCACAACCTGAGGCTATTAACAAAGTCTTCTGGA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTCACAACCTGAGGCTATTAACAAAGTCTTCTGGA	3420
Qy	3421	GTAATTTGTAAGCATCTCGTAATTAATAAAGCAAGAAATATGAAGAGTAGTTCAACTGTTA	3480

Db	3421	GTAAATTGACAGTCCCTGAAATTAATAAGCAAGAAATATGAAGAAGTACCTTCAAGCTCTTA	3480
Qy	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACACGCTTAGGGAAATAGTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACACGCTTAGGGAAATAGTC	3540
Qy	3541	ATGCATCTCAGGTTTGTTCTTGAGACCTGTGATGACCTGTTAGATGATGGTGAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTTCTTGAGACCTGTGATGACCTGTTAGATGATGGTGAATTAAGG	3600
Qy	3601	AAGATACTAGTTTGTGCTGAAATAACATTAAGAAAGTCTGCTGTTTAAAGCAAAAGCG	3660
Db	3601	AAGATACTAGTTTGTGCTGAAATAACATTAAGAAAGTCTGCTGTTTAAAGCAAAAGCG	3660
Qy	3661	TCCAGAAAGAGAGCTTAGACAGAGTCCTAGACCCCTTTCACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGAGAGCTTAGACAGAGTCCTAGACCCCTTTCACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTACCGAAGAGGGGCCCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTGAGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCCAAGAAATTAGAGTCTCAGAAAGAACTTATCTAGTGAGAGATG	3780
Qy	3781	AAGAGCTCCCGTCTCCACACTTGTTATTTGGTAAAGTAAACAATATCCTTCAGT	3840
Db	3781	AAGAGCTCCCGTCTCCACACTTGTTATTTGGTAAAGTAAACAATATCCTTCAGT	3840
Qy	3841	CTACTAGGCATAGACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTGAAGATAGCTTAATAATGATCTGACGTAAACCAAGTATATTGGCAAGGCATCTC	3960
Db	3901	TATCATTGAAGATAGCTTAATAATGATCTGACGTAAACCAAGTATATTGGCAAGGCATCTC	3960
Qy	3961	AGGAACATCACCCTTAGTAGAGGAAACAAATGTTGTGTAGCTGTTTCTTCAACAGTCA	4020
Db	3961	AGGAACATCACCCTTAGTAGAGGAAACAAATGTTGTGTAGCTGTTTCTTCAACAGTCA	4020
Qy	4021	GTGAATTGGAAGACTTGACTGCAATATCAAAACCCAGAGATCCCTTCTTGATGGTTCCTT	4080
Db	4021	GTGAATTGGAAGACTTGACTGCAATATCAAAACCCAGAGATCCCTTCTTGATGGTTCCTT	4080
Qy	4081	CCAAACAAATAGGCATCAGTCTGAAAACCGAGGAGTTGGTCTGAGTGAACAAGAAATTTGG	4140
Db	4081	CCAAACAAATAGGCATCAGTCTGAAAACCGAGGAGTTGGTCTGAGTGAACAAGAAATTTGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATTAATCAAGAACACAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATTAATCAAGAACACAAAGCA	4200
Qy	4201	TGGAATTCAAACTTTAGGTGAACACACTCTGGGCTGAGAGTGAACAAGGCTCTCTGAAG	4260
Db	4201	TGGAATTCAAACTTTAGGTGAACACACTCTGGGCTGAGAGTGAACAAGGCTCTCTGAAG	4260
Qy	4261	ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAACTCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAACTCACTCAGCAGAGGATACCATGC	4320
Qy	4321	AACATTAACCTGATTAAGTCTCAGCAGAAATGGCTGAACCTAGAAAGCTGTATTGAACAGC	4380
Db	4321	AACATTAACCTGATTAAGTCTCAGCAGAAATGGCTGAACCTAGAAAGCTGTATTGAACAGC	4380
Qy	4381	ATGGAGGACGCTTCTTAACAGCTAAGCTTCATCATTAAGTGACTCTTCTGCGCTTGAGG	4440
Db	4381	ATGGAGGACGCTTCTTAACAGCTAAGCTTCATCATTAAGTGACTCTTCTGCGCTTGAGG	4440
Qy	4441	ACCTGCGAAATCCAGAACCAAGCACATCAGAAAAAGCAGATTAACTTCAACAGAAAAATG	4500
Db	4441	ACCTGCGAAATCCAGAACCAAGCACATCAGAAAAAGCAGATTAACTTCAACAGAAAAATG	4500
Qy	4501	GTGAATACCTTAATAGCCAGATTCAGAGGCTTTTCTGCTGAACAGTTTGAGGTCTG	4560
Db	4501	GTGAATACCTTAATAGCCAGATTCAGAGGCTTTTCTGCTGAACAGTTTGAGGTCTG	4560

QY 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGSAACTGTCTCCAAAGTGTGACC 240
DB 181 TCTTAAAGAGTGTCCCATCTGTCTGAGATTGATCAAGSAACTGTCTCCAAAGTGTGACC 240
QY 241 ACATATTTTGGCAAAATTTTGATGCTGAACTTCTCAACCGAAGAAAGGGCTTCAAGT 300
DB 241 ACATATTTTGGCAAAATTTTGATGCTGAACTTCTCAACCGAAGAAAGGGCTTCAAGT 300
QY 301 GTCCCTTATGTAGAAATGATATATACCAAAAGAGCCCTACAGAAAGTACAGATTTTATGTC 360
DB 301 GTCCCTTATGTAGAAATGATATATACCAAAAGAGCCCTACAGAAAGTACAGATTTTATGTC 360
QY 361 AACTGTGTGAAGAGCTATTTGAAATCAATTTGTCTTTTCAAGCTTGACACAGTTTGGAGT 420
DB 361 AACTGTGTGAAGAGCTATTTGAAATCAATTTGTCTTTTCAAGCTTGACACAGTTTGGAGT 420
QY 421 ATGCAAAACGCTATATTTTGGCAAAAGGAAATACTCTCTGAAACATCTTAAAGATG 480
DB 421 ATGCAAAACGCTATATTTTGGCAAAAGGAAATACTCTCTGAAACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGATGAGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGATGAGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540
QY 541 AACCCCAAAATCCTTCTCTGAGAAACCAAGTCTCAAGTCTCAACTCTCTAACCTTGGAA 600
DB 541 AACCCCAAAATCCTTCTCTGAGAAACCAAGTCTCAAGTCTCAACTCTCTAACCTTGGAA 600
QY 601 CTGTGAGAACTCTGAGGACAAAGACAGCGATACAACTCTCAAAAGAGCTGTCTACATG 660
DB 601 CTGTGAGAACTCTGAGGACAAAGACAGCGATACAACTCTCAAAAGAGCTGTCTACATG 660
QY 661 AATTTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTCAGTGTGGAG 720
DB 661 AATTTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTCAGTGTGGAG 720
QY 721 ATCAAAATTTGTACAAATACACCCCTCAAGGAAACCAAGGATGAATCACTTTGGATTCTG 780
DB 721 ATCAAAATTTGTACAAATACACCCCTCAAGGAAACCAAGGATGAATCACTTTGGATTCTG 780
QY 781 CAAAAAAGGCTGTCTGGAATTTTCTGAGACGAGTGAACAAATATCTGAACATCATCAAC 840
DB 781 CAAAAAAGGCTGTCTGGAATTTTCTGAGACGAGTGAACAAATATCTGAACATCATCAAC 840
QY 841 CCAGTAATATATGATTTTGAACACCACTGAGAAAGCTGAGTGAAGGATCCAGAAAGT 900
DB 841 CCAGTAATATATGATTTTGAACACCACTGAGAAAGCTGAGTGAAGGATCCAGAAAGT 900
QY 901 ATAGAGGATGTTCTGTTTCAAACTTGTGATGAGACCATGTGGCAAAATATCTGATGCCA 960
DB 901 ATAGAGGATGTTCTGTTTCAAACTTGTGATGAGACCATGTGGCAAAATATCTGATGCCA 960
QY 961 GCTCATTAACAGCATGAGAACAGCATTTTATTACTCACTAAAGACAAATGATGTAAGAA 1020
DB 961 GCTCATTAACAGCATGAGAACAGCATTTTATTACTCACTAAAGACAAATGATGTAAGAA 1020
QY 1021 AGGCTGAATTTCTGTATTAATAAGCAAAACAGCTGGCTTAGCAAGAACCAATATACAGAT 1080
DB 1021 AGGCTGAATTTCTGTATTAATAAGCAAAACAGCTGGCTTAGCAAGAACCAATATACAGAT 1080
QY 1081 GGGCTGAAGATGAGAAACATGTAAATGAGGCGGACTCCAGACACAGAAAGAAAGGTAG 1140
DB 1081 GGGCTGAAGATGAGAAACATGTAAATGAGGCGGACTCCAGACACAGAAAGAAAGGTAG 1140
QY 1141 ATCTGATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGAGAAATCTGCTATGCT 1200
DB 1141 ATCTGATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGAGAAATCTGCTATGCT 1200
QY 1201 CAGAGAAATCTTAGAGATCTGAAGATGTTCTTGTGATACACTTAATATAGCAGATTCAG 1260
DB 1201 CAGAGAAATCTTAGAGATCTGAAGATGTTCTTGTGATACACTTAATATAGCAGATTCAG 1260

QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACGTGTTAGTCTGATGATCAGATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACGTGTTAGTCTGATGATCAGATGATG 1320
QY 1321 GGGAGTCTGAATCAATATGCAAGAGTATGATATTTGACGTTCTAAATGAGATGATG 1380
DB 1321 GGGAGTCTGAATCAATATGCAAGAGTATGATATTTGACGTTCTAAATGAGATGATG 1380
QY 1381 AATATTTCTGTTCTTACAGAAATAATGATTTCTGCGCAGTATCTCTACAGGCTTTAA 1440
DB 1381 AATATTTCTGTTCTTACAGAAATAATGATTTCTGCGCAGTATCTCTACAGGCTTTAA 1440
QY 1441 TATGTAAAGTAAAGAGTGTCTCCAAATCAGTAGAGTAAATTTGAGACAAATAT 1500
DB 1441 TATGTAAAGTAAAGAGTGTCTCCAAATCAGTAGAGTAAATTTGAGACAAATAT 1500
QY 1501 TTGGGAAAACTATGAGAAAGGAGAGGAGCTCCCACTTAAGCATGATGAAATATC 1560
DB 1501 TTGGGAAAACTATGAGAAAGGAGAGGAGCTCCCACTTAAGCATGATGAAATATC 1560
QY 1561 TAATTAATGAGACATTTGTTACTGAGCCACAGATTAATACAGAGGTCCTTCACAATA 1620
DB 1561 TAATTAATGAGACATTTGTTACTGAGCCACAGATTAATACAGAGGTCCTTCACAATA 1620
QY 1621 AATTAAGGCTAAAGAGACCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
DB 1621 AATTAAGGCTAAAGAGACCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTTGGCAGATTCAAAAGACCTCTGAAATGATTAATCAGGAACTAAACCAACGAGAC 1740
DB 1681 CAGATTTTGGCAGATTCAAAAGACCTCTGAAATGATTAATCAGGAACTAAACCAACGAGAC 1740
QY 1741 AGAATGTCATAGTGAATATTAATTAATGTCATAGAGATTAATAACAAAGGATG 1800
DB 1741 AGAATGTCATAGTGAATATTAATTAATGTCATAGAGATTAATAACAAAGGATG 1800
QY 1801 CTATTCAGATGAGAAATAATCTTAACCCATGGAATCACTCGAAAAAGAAATCGCTTTCA 1860
DB 1801 CTATTCAGATGAGAAATAATCTTAACCCATGGAATCACTCGAAAAAGAAATCGCTTTCA 1860
QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGACAGTATTAAGCAATATGGAATCGAATTAATATCC 1920
DB 1861 AAAAGAAAGCTGAACCTATTAAGCAGACAGTATTAAGCAATATGGAATCGAATTAATATCC 1920
QY 1921 ACAAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGGAAAGTCTTCTACAGGCAATATTC 1980
DB 1921 ACAAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGGAAAGTCTTCTACAGGCAATATTC 1980
QY 1981 ATGCGCTGAACTAGTACAGTACAGTAAATCTAAGCCACCTAATGTACTGAATGCAAA 2040
DB 1981 ATGCGCTGAACTAGTACAGTACAGTAAATCTAAGCCACCTAATGTACTGAATGCAAA 2040
QY 2041 TTGATAGTGTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAATATGCCAGTCA 2100
DB 2041 TTGATAGTGTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAATATGCCAGTCA 2100
QY 2101 GGCACAGCAAAACCTACATCATGAGAAAGGTAAGAACTTCACTGAGGCCAAGAA 2160
DB 2101 GGCACAGCAAAACCTACATCATGAGAAAGGTAAGAACTTCACTGAGGCCAAGAA 2160
QY 2161 GTAAACAGCAAAATGAACAGACAGTAAAGACATGACAGGATATCTTCCAGAGCTGA 2220
DB 2161 GTAAACAGCAAAATGAACAGACAGTAAAGACATGACAGGATATCTTCCAGAGCTGA 2220
QY 2221 AGTTAACAAATGACCTGTGTTCTTTTACTAAGTGTCAAAATACAGTGAATTTAAAGAT 2280
DB 2221 AGTTAACAAATGACCTGTGTTCTTTTACTAAGTGTCAAAATACAGTGAATTTAAAGAT 2280
QY 2281 TTGTCAATCTTACGCTTCCAAAGAGAAAGAAAGAAAGAAATAGAAACAGTTAAAGTGT 2340
DB 2281 TTGTCAATCTTACGCTTCCAAAGAGAAAGAAAGAAAGAAAGAAAGTTAAAGTGT 2340
QY 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTAAATGAGAAAGGTTTGGCAAACTG 2400

OY	2641	GGGAAACAAGATGTGAAATGGAAAGAAAGTGAACCTGATGCTCACTATTTGGAGAAATCAT	2700
Db	2641	GGGAAACAAGATGTGAAATGGAAAGAAAGTGAACCTGATGCTCACTATTTGGAGAAATCAT	2700
OY	2701	TCAGAGTTTCAAAGCGCCAGTCATTGGTCTGTTTTCAATCCAGAAATGCGAAGAGG	2760
Db	2701	TCAGAGTTTCAAAGCGCCAGTCATTGGTCTGTTTTCAATCCAGAAATGCGAAGAGG	2760
OY	2761	AATGTGCAACATTCTCTGCCCCACCTCTGGGTCCTTTAAAGAAACCAAGTCACCTT	2820
Db	2761	AATGTGCAACATTCTCTGCCCCACCTCTGGGTCCTTTAAAGAAACCAAGTCACCTT	2820
OY	2821	TTGAAATGGAACAAAAGGAAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAAATGGAACAAAAGGAAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCTGTAC	2880
OY	2881	AGACAGTTAATATCATCTGACAGGCTTCTGTGGTTGGTCAGAAAGATPAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCATCTGACAGGCTTCTGTGGTTGGTCAGAAAGATPAAGCCAGTTGATA	2940
OY	2941	ATGCGCAATGTAAATATCAAAAGAGCTCTAGCTTTGTCTATCTCAGTTCAGAGCA	3000
Db	2941	ATGCGCAATGTAAATATCAAAAGAGCTCTAGCTTTGTCTATCTCAGTTCAGAGCA	3000
OY	3001	ACGAAACCTGACCTATTCTCTCAAAATAAACATGAGCTTTTACAAACCCATATGCTATAC	3060
Db	3001	ACGAAACCTGACCTATTCTCTCAAAATAAACATGAGCTTTTACAAACCCATATGCTATAC	3060
OY	3061	CACCACTTTTCCCATCAAGTCATTGTTTAAACTAAATGTAAAGAAAATCTGCTAGAG	3120
Db	3061	CACCACTTTTCCCATCAAGTCATTGTTTAAACTAAATGTAAAGAAAATCTGCTAGAG	3120
OY	3121	AAAACCTTGGAGAAACATTCAATGTACCTGAAAGAGAAATGGAAATGAGAACTTCCAA	3180
Db	3121	AAAACCTTGGAGAAACATTCAATGTACCTGAAAGAGAAATGGAAATGAGAACTTCCAA	3180
OY	3181	GTCAGTGAGCACAATTAGCCGCTAATAACATTAGAGAAAATGTTTTTAAAGAACCCAGCT	3240
Db	3181	GTCAGTGAGCACAATTAGCCGCTAATAACATTAGAGAAAATGTTTTTAAAGAACCCAGCT	3240
OY	3241	CAAGCAATATTAATGAACATAGTTCACGACTAATAATGAATGGGCTCCAGTATTATGAA	3300
Db	3241	CAAGCAATATTAATGAACATAGTTCACGACTAATAATGAATGGGCTCCAGTATTATGAA	3300
OY	3301	TAGGTTCCAGTGATGAAGAAACATTCAGAGAGAACTAGTAGAGAAACAGAGGCGCAAAATTTGA	3360
Db	3301	TAGGTTCCAGTGATGAAGAAACATTCAGAGAGAACTAGTAGAGAAACAGAGGCGCAAAATTTGA	3360
OY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATTAACAAAGTCTTCTTGAAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATTAACAAAGTCTTCTTGAAA	3420
OY	3421	GTAATTTGAACATCTCGAAATTAAGAAAGCAAGAAATGAAGAGTGGTTGAGCTGTTA	3480
Db	3421	GTAATTTGAACATCTCGAAATTAAGAAAGCAAGAAATGAAGAGTGGTTGAGCTGTTA	3480
OY	3481	ATACAGATTTCTTCCATATCTGATTTGAGATTAACCTTAAGAACAGCTATGGGAAGTAGTC	3540
Db	3481	ATACAGATTTCTTCCATATCTGATTTGAGATTAACCTTAAGAACAGCTATGGGAAGTAGTC	3540
OY	3541	ATGCACTTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGCTGAATTAAGG	3600
Db	3541	ATGCACTTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGCTGAATTAAGG	3600
OY	3601	AAGATACTAGTTTGTCTGAGAAATGACATTAAGAAAGTTCTGCTGTTTTTGAACAAAGCG	3660
Db	3601	AAGATACTAGTTTGTCTGAGAAATGACATTAAGAAAGTTCTGCTGTTTTTGAACAAAGCG	3660
OY	3661	TCGAGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACCCATATACATTTGGCTCAGG	3720
Db	3661	TCGAGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACCCATATACATTTGGCTCAGG	3720

QY	3721	CTTACCGAAGGGGGCCAAAGAAATTAAAGTCCCTCAGAAAGAACTTTTCTAAGAGGATG	3780
Db	3721	GTTACCGAAGGGGGCCAAAGAAATTAAAGTCCCTCAGAAAGAACTTTTCTAAGAGGATG	3780
QY	3781	AAGAGCTTCCCTGGCTTCCAAACACTTGTATTGTGTAAGTAACAAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGGCTTCCAAACACTTGTATTGTGTAAGTAACAAATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGTGTCTACCGAGTGTCTGTCTTAAGAACACAGAGAGCAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGTGTCTACCGAGTGTCTGTCTTAAGAACACAGAGAGCAATTTAT	3900
QY	3901	TATCATTAAGAAATAGCTTAAATTAAGTACGACATACCAAGTAAATTTGGCAAAAGCATCTC	3960
Db	3901	TATCATTAAGAAATAGCTTAAATTAAGTACGACATACCAAGTAAATTTGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTGAAGGAAACAAATGTCTGTACTGTTTCTTCAACGTGCA	4020
Db	3961	AGGAACATCACCTTAGTGAAGGAAACAAATGTCTGTACTGTTTCTTCAACGTGCA	4020
QY	4021	GTTGAATTGGAAGACTGATCGTCAAAATCAACACCGAGAACTCTTCTGTATTTGGTCTT	4080
Db	4021	GTTGAATTGGAAGACTGATCGTCAAAATCAACACCGAGAACTCTTCTGTATTTGGTCTT	4080
QY	4081	CCAAACAAATAGGCATAGTCTGAAAGCCAGGAGTTGTCTGAGTGCACAGCAATTTGG	4140
Db	4081	CCAAACAAATAGGCATAGTCTGAAAGCCAGGAGTTGTGTGAGTGCACAGCAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGGAAACGGGCTTGGAAAGAAATATCAAGAGAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAAACGGGCTTGGAAAGAAATATCAAGAGAGCAAGCA	4200
QY	4201	TGGATTCAAACTTATAGTGAAGCACACTCTGTGGTGTGAGAGTGAACAAGACGTCTCTGAAG	4260
Db	4201	TGGATTCAAACTTATAGTGAAGCACACTCTGTGGTGTGAGAGTGAACAAGACGTCTCTGAAG	4260
QY	4261	ACTGCTCAGGCTTATCTCTCAGAGTGCATTTTAAACAACCTCAGCAAGGAGTATCCATGC	4320
Db	4261	ACTGCTCAGGCTTATCTCTCAGAGTGCATTTTAAACAACCTCAGCAAGGAGTATCCATGC	4320
QY	4321	AAACATTAACCTATTAAGTCCAGAGAGGAAATGGCTGAACCTGAAGCTGTGTAAACAGC	4380
Db	4321	AAACATTAACCTATTAAGTCCAGAGAGGAAATGGCTGAACCTGAAGCTGTGTAAACAGC	4380
QY	4381	ATGGAGGCACAGCTTCTTAACAGCTAACCCCTTCATCATAGTACTCTTCTGSCCTTGAGG	4440
Db	4381	ATGGAGGCACAGCTTCTTAACAGCTAACCCCTTCATCATAGTACTCTTCTGSCCTTGAGG	4440
QY	4441	ACCTGCGAAATCCAGAACCAAGGACATTCAGAAAAAGCAAGTATTAACCTTCAACAGAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACCAAGGACATTCAGAAAAAGCAAGTATTAACCTTCAACAGAAAGTA	4500
QY	4501	GTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTTGAGGTCTG	4560
Db	4501	GTGAATACCTTATTAAGCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTTGAGGTCTG	4560
QY	4561	CAGATAGTTCTAACGATTAATAATTAAGAACCCAGAGTGAAGAAAGTCAATCCCTCTCTAAT	4620
Db	4561	CAGATAGTTCTAACGATTAATAATTAAGAACCCAGAGTGAAGAAAGTCAATCCCTCTCTAAT	4620
QY	4621	GCCCATCATTTAGATATAGTGTGATGCAGTGCAGTGTCTGGAGAGTCTTACAGAAATGAA	4680
Db	4621	GCCCATCATTTAGATATAGTGTGATGCAGTGCAGTGTCTGGAGAGTCTTACAGAAATGAA	4680
QY	4681	ACTACCCATCTCAAGAGAGGCTCATTAAGTGTGTAATGTGAGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTACCCATCTCAAGAGAGGCTCATTAAGTGTGTAATGTGAGAGAGCAACAGCTGGAAG	4740
QY	4741	AGTCTGGGSCACAGATTTGAAGGAAACATTTTACTTGCCAAAGCAAGATTTGAAGGGA	4800
Db	4741	AGTCTGGGSCACAGATTTGAAGGAAACATTTTACTTGCCAAAGCAAGATTTGAAGGGA	4800
QY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTCGAATCTGATCCTTCTG	4860

Db 421 ATGAAAAGCTATATATTTTGCAAAAGAAAATAAATCTCTGAAACATTAAGAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGATATGGGCTACAGAAACGGTSCCAAAAGACTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGATATGGGCTACAGAAACGGTSCCAAAAGACTTCTACAGAGTG 540
Qy 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTAGTGTCCAACTCTTAACTTGA 600
Db 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTAGTGTCCAACTCTTAACTTGA 600
Qy 601 CTGTGAGAACTCTGAGACCAAGACGGATACAACTTAAAGAGCTGTGTCTACATTG 660
Db 601 CTGTGAGAACTCTGAGACCAAGACGGATACAACTTAAAGAGCTGTGTCTACATTG 660
Qy 661 AATTGGAGCTGATCTCTGAGAAATCCGTTAATAGGCACTTATTGACGTGGAG 720
Db 661 AATTGGAGCTGATCTCTGAGAAATCCGTTAATAGGCACTTATTGACGTGGAG 720
Qy 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGAACCAAGGATGAAATCAGTTTGAATTCTG 780
Db 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGAACCAAGGATGAAATCAGTTTGAATTCTG 780
Qy 781 CAAAAAGGCTGCTTGTGATTTTCTGAGACGGATGTAACTGAACTGAACTCACTAAC 840
Db 781 CAAAAAGGCTGCTTGTGATTTTCTGAGACGGATGTAACTGAACTGAACTCACTAAC 840
Qy 841 CCAGTAATATGATTTTGAACACCACTGAGAAACGTGAGAGGCACTCCAGAAAGT 900
Db 841 CCAGTAATATGATTTTGAACACCACTGAGAAACGTGAGAGGCACTCCAGAAAGT 900
Qy 901 ATCAGGGTAGTCTGTCTTCAACTTGATGAGACCAATGTGGCAAAATATCTCATGCA 960
Db 901 ATCAGGGTAGTCTGTCTTCAACTTGATGAGACCAATGTGGCAAAATATCTCATGCA 960
Qy 961 GCTATTTACAGCATGAGAAACAGCAGTTTATTACTCACTAAGACAGAAATGATGAAA 1020
Db 961 GCTATTTACAGCATGAGAAACAGCAGTTTATTACTCACTAAGACAGAAATGATGAAA 1020
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Db 1021 AGGCTGAATTTCTGTATATAAAGCAAAACAGCTGCTTGAAGAGGCCAACTAATCAGAT 1080
Qy 1081 GGGCTGGAAGTAAAGGAAACATGTATATGATAGCGGACCTCCAGCACAGAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTAAAGGAAACATGTATATGATAGCGGACCTCCAGCACAGAAAAAGGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAAAGAAATGAAATAGCAGAACTGCGATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAAAGAAATGAAATAGCAGAACTGCGATGCT 1200
Qy 1201 CAGAGAAATCTAGAGATCTAGAGATGTTTCTTGATTAACACTTAATATGACAGATTCAGA 1260
Db 1201 CAGAGAAATCTAGAGATCTAGAGATGTTTCTTGATTAACACTTAATATGACAGATTCAGA 1260
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTATGAACCTGTAGGTTCTGATGACTCAATGATG 1320
Db 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTATGAACCTGTAGGTTCTGATGACTCAATGATG 1320
Qy 1321 GGGAGTCTGAATCAAAAGCCAAAGTATGATGTTTGAAGCGTTCTAAATGAGGTAGATG 1380
Db 1321 GGGAGTCTGAATCAAAAGCCAAAGTATGATGTTTGAAGCGTTCTAAATGAGGTAGATG 1380
Qy 1381 AATATTTCTGTTCTTCCAGAGAAATAGACTTACTGGCAGATGCTCATGAGGCTTTAA 1440
Db 1381 AATATTTCTGTTCTTCCAGAGAAATAGACTTACTGGCAGATGCTCATGAGGCTTTAA 1440
Qy 1441 TATGTAAAGTGAAGAGTCTCACTCAATCAGTAGAGATATATTTGAAGCAAAATAT 1500
Db 1441 TATGTAAAGTGAAGAGTCTCACTCAATCAGTAGAGATATATTTGAAGCAAAATAT 1500
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAAAATC 1560
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Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAAAATC 1560
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Db 1561 TAATTAATGAGCACTTTGTTACTGAGCCACAGATATATACAAGACGTCCTCCACAAATA 1620
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Qy 1681 CAGATTTGGGAGTTCAAAAAGCTCTGTAATGATTAATTCAGGAACTTAACCAAGAGC 1740
Db 1681 CAGATTTGGGAGTTCAAAAAGCTCTGTAATGATTAATTCAGGAACTTAACCAAGAGC 1740
Qy 1741 AGAATGCTCAGATGATTAATTAATATAGTGTCTGAGAAATTAACCAAGAGTATTC 1800
Db 1741 AGAATGCTCAGATGATTAATTAATATAGTGTCTGAGAAATTAACCAAGAGTATTC 1800
Qy 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860
Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860
Qy 1861 AAAGGAAAGCTGAACCTTAAAGCAGCAGTAAAGCAATAGGAACTGAAATTAATATTC 1920
Db 1861 AAAGGAAAGCTGAACCTTAAAGCAGCAGTAAAGCAATAGGAACTGAAATTAATATTC 1920
Qy 1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAGTCTTCAACGAGCATATTC 1980
Db 1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAGTCTTCAACGAGCATATTC 1980
Qy 1981 ATGGGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCCACTTAATGTACTGAATTCGAAA 2040
Db 1981 ATGGGCTTGAACCTAGTAGTCAAGTAAATCTAAGCCCACTTAATGTACTGAATTCGAAA 2040
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Db 2041 TTGATAGTGTCTTCAAGAGTGAAGAGTAAAGAAAAAAAGTCAACCAATATCCAGTCA 2100
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Db 2101 GGCACAGCAGAAACCTTCAACTCACTGAGAAAGTAAAGAACTGGAACCTGAGCCAAAGAG 2160
Qy 2161 GTAAACAAGCCAAATGAACAGACAAATGAAGACATGACAGGATCTTCCAGAGCTGA 2220
Db 2161 GTAAACAAGCCAAATGAACAGACAAATGAAGACATGACAGGATCTTCCAGAGCTGA 2220
Qy 2221 AGTTAAACAATGACACCTGTGTTCTTTACTAAGTGTCAATATACCATGAACTTAAAGAT 2280
Db 2221 AGTTAAACAATGACACCTGTGTTCTTTACTAAGTGTCAATATACCATGAACTTAAAGAT 2280
Qy 2281 TTGTCAATCTAGGCTTCCAAAGAGAGAAAAAGAGAACTGAGAAACGTTAAAGTGT 2340
Db 2281 TTGTCAATCTAGGCTTCCAAAGAGAGAAAAAGAGAACTGAGAAACGTTAAAGTGT 2340
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400
Qy 2401 AAAAGTCTGTAAGAGTAGAGATTTCAATTTGATCTGTAATGCACTGACACAG 2460
Db 2401 AAAAGTCTGTAAGAGTAGAGATTTCAATTTGATCTGTAATGCACTGACACAG 2460
Qy 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGAGAAAGCAAAACAGAAACCAATTAAT 2520
Db 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGAGAAAGCAAAACAGAAACCAATTAAT 2520
Qy 2521 GTGTAGTCAAGTGTGACATTTGAAAACCCCAAGGACCTAATTCATGTTGTTCCAAAG 2580
Db 2521 GTGTAGTCAAGTGTGACATTTGAAAACCCCAAGGACCTAATTCATGTTGTTCCAAAG 2580
Qy 2581 ATATATAGAAATGACACAGAAAGCTTTAAGTATCATTTGGGACATGAAGTTAACACACATC 2640
Db 2581 ATATATAGAAATGACACAGAAAGCTTTAAGTATCATTTGGGACATGAAGTTAACACACATC 2640

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 Db 3061 CACCACTTTTCCCATCAAGTATTTGTTAAATGTAAGAAAAATCTGCTAGAG 3120
 QY 3121 AAAAATTGAGGAACTTCAATGTCACCTGAAAGAAATGGAAATGGAACATTTCCA 3180
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 QY 3601 AAGATTAAGTATGCTGATAAATGACATTAAGGAAGTCTGCTGTTTGAAGCAAAACG 3660
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 QY 3841 CTACTAGGATAGCAACCGTGTGACCGAGTGTCTGTCTAAGAAACAGAGAGAAATTTAT 3900
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 QY 3901 TATCATTAAGAAATTAAGTAAATGCTGACAGTAACAGGTAATATTTGCAAAAGCATCTC 3960
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Qy 901 ATAGAGGTGTTCTGTTTCAACTGTGATGTGAGGCATGTGGCACAAAATACTCATGCCA 960
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Db 1921 ACAATTTCAAAGACCTTAAGAAATAGGCTGAGAGAGAGTCTTCTACAGGCATATTC 1980
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Qy 2401 AAAAGTCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
Db 2401 AAAAGTCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
Qy 2461 AAAAGTCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Db 2461 AAAAGTCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
Qy 2521 GTGTGAGTCAAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 2521 GTGTGAGTCAAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
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Db 2581 ATATATGAAATGACACAGAGAGCTTAAATATCATTTGGGACATGAAGTTAACACAGTC 2640
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Db 2641 GGGAAACAGCATGAGAAATGGAAGAGTGAATGCTGATGATGATGATGATGATGATGAT 2700
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DB 5521 GCACAGGTGTCACCCCAATTTGTTGTGACACCAATCCCTGAGACAGACATGAGCT 5580
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DB 5581 TCCATGCAATTTGGAGAGATGTGTGAGAGCACTGTGTGACCCGAGAGTGGTGTGACA 5640
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DB 5641 GTGTGACACTTACCAAGTGGCAGAGCTGAGACACCTACTGATACCCAGATCCCCACA 5700
QY 5701 GCCCACTACTGA 5711
DB 5701 GCCCACTACTGA 5711

RESULT 13

AAT32601 standard: cDNA, 5914 BP.

AC AAT32601;
XX 19-NOV-1996 (first entry)
DE BRCA1, breast and ovarian cancer susceptibility gene.
XX BRCA1, breast cancer; ovarian cancer; predisposing gene; diagnosis;
KM susceptibility gene; prognosis; gene therapy; ds.
XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 120..5711
FT /*tag=a
FT /product= BRCA1 protein

XX W09605308-A1.

XX 22-FEB-1996.
XX 11-AUG-1995; 95WO-US10220.

XX 07-JUN-1995; 95US-0488011.
XX 12-AUG-1994; 94US-0289221.
XX 02-SEP-1994; 94US-0300266.
XX 16-SEP-1994; 94US-0308104.
XX 29-NOV-1994; 94US-0348824.
XX 24-MAR-1995; 95US-0409305.
XX 07-JUN-1995; 95US-0483554.
XX 07-JUN-1995; 95US-0487002.

XX (MYRI-) MYRIAD GENETICS INC.
XX (UTAH) UNIV UTAH RES FOUND.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Futreal PA, Goldgar DE, Harshman KD, Kamb A, Miki Y;
XX Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;
XX Wiseman RW;

XX WPI, 1996-139704/14.

XX P-PSDB; AAR97128.

XX New method for diagnosing a predisposition to breast and ovarian
XX cancer - by detecting a germline alteration in the BRCA1 gene or
XX PT gene regulatory sequence; for gene therapy and to screen for drugs
XX PS Claim 4; Page 108-117; 200pp; English.

CC This is the nucleotide sequence of the breast and ovarian cancer
CC susceptibility gene, BRCA1. Four kindred families provided genetic
CC evidence for localization of BRCA1 to a sufficiently small region for
CC the application of positional cloning strategies. A detailed map of
CC transcripts was developed for the region of 17q21 between D17S1321 and
CC D17S1324. A combination of sequences obtained from cDNA clones,
CC hybrid-selected sequences and PCR products, allowed construction of a
CC composite full-length BRCA1 cDNA (see AAT32612 for genomic sequence).
CC The isolated cDNA is used in methods for either diagnosis of the
CC predisposition to cancer (partic. breast and ovarian cancer), or for the
CC diagnosis or prognosis of cancer, and also in gene-based therapies
CC directed at cancer cells.

XX Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 17; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTCTGACACCCGACAGGCTGTGGGTTTCTGATTAACCTGGGCC 60
DB 1 AGCTGCTGAGACTTCTCTGACACCCGACAGGCTGTGGGTTTCTGATTAACCTGGGCC 60
QY 61 CTTGGGCTCAGAGAGGCTTCACTCTGTCTGTGGGTAAAGTTCAATGGAACAGAAAGAA 120
DB 61 CTTGGGCTCAGAGAGGCTTCACTCTGTCTGTGGGTAAAGTTCAATGGAACAGAAAGAA 120
QY 121 TGGATTTATCTGCTCTTGGGCTTGAAGAAGTAAATGATTAATGATTAATGATTAATG 180
DB 121 TGGATTTATCTGCTCTTGGGCTTGAAGAAGTAAATGATTAATGATTAATGATTAATG 180
QY 181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAAGCTGTCTCCACAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAAGCTGTCTCCACAAAGTGTGACC 240
QY 241 ACATATTTTGGCAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGSCCTTCAAGT 300
DB 241 ACATATTTTGGCAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGSCCTTCAAGT 300
QY 301 GTCCCTTATGTAAGAATGATTAACCAAGAAGGCTTCAAGAAGTGAAGATTAATGTC 360
DB 301 GTCCCTTATGTAAGAATGATTAACCAAGAAGGCTTCAAGAAGTGAAGATTAATGTC 360
QY 361 AACTGTGTAAGAGCTATTGAAATCATTTGTGCTTTACGTGACACAGTTTGGAGT 420
DB 361 AACTGTGTAAGAGCTATTGAAATCATTTGTGCTTTACGTGACACAGTTTGGAGT 420
QY 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTGTAACATTAAGATG 480
DB 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTGTAACATTAAGATG 480
QY 481 AAGTTTCATGATCAAGATTAAGGCTGACAGAAACCGTGCAGAAAGCTTCTACAGAGT 540
DB 481 AAGTTTCATGATCAAGATTAAGGCTGACAGAAACCGTGCAGAAAGCTTCTACAGAGT 540
QY 541 AACCAGAAATCTCTCTCTGAGGAAACAGCTCTCACTCTCTAACCCTTGAA 600
DB 541 AACCAGAAATCTCTCTCTGAGGAAACAGCTCTCACTCTCTAACCCTTGAA 600
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGGATTAACCTCAAAAGAGCTGTCTACATTG 660
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGGATTAACCTCAAAAGAGCTGTCTACATTG 660
QY 661 AATGGAGATCGATTTCTTGAAGATTAAGTAAAGGCACTTAATGAGAGTGGAG 720
DB 661 AATGGAGATCGATTTCTTGAAGATTAAGTAAAGGCACTTAATGAGAGTGGAG 720
QY 721 ATCAAGATTTGTAACATCAACCCCTCAAGGATCAAGGATGAATCAAGTTGGATTCTG 780
DB 721 ATCAAGATTTGTAACATCAACCCCTCAAGGATCAAGGATGAATCAAGTTGGATTCTG 780
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGAACAAATGATGAACATCAAC 840
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGAACAAATGATGAACATCAAC 840

Db 3241 CAAGCAATAATTAAGTAGAGTTCCAGTACTAATGAAGTGGGCTCAGATTAATGA 3300
QY 3301 TAGGTTCCAGTGTATGAATACTTCAGCAGAACTAGTAGAAACAGAGGGCCAAATTTGA 3360
Db 3301 TAGGTTCCAGTGTATGAATACTTCAGCAGAACTAGTAGAAACAGAGGGCCAAATTTGA 3360
QY 3361 ATGCTATGCTTAGATTAAGGGGTTTTGCAACTGAGGCTTAATAACAAGTCTTCTGGA 3420
Db 3361 ATGCTATGCTTAGATTAAGGGGTTTTGCAACTGAGGCTTAATAACAAGTCTTCTGGA 3420
QY 3421 GTAATTGTAAAGCATCTCTGAATAAAGCAAGAAATATGAAGAAGTAGTTCAAGCTTTA 3480
Db 3421 GTAATTGTAAAGCATCTCTGAATAAAGCAAGAAATATGAAGAAGTAGTTCAAGCTTTA 3480
QY 3481 ATACCAATTTCTCCATATCTGATTTTCAGATACTTAAGAACGCTTAAGGAAGTAGTC 3540
Db 3481 ATACCAATTTCTCCATATCTGATTTTCAGATACTTAAGAACGCTTAAGGAAGTAGTC 3540
QY 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGTAATAAG 3600
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QY 3601 AAGATATAGTTTGTCTGAATAATGACATTAAGAAAATTCTGCTGTTTGAACAAAGCG 3660
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QY 3661 TCCAGAAAGAGGCTTAGCAGAGATCTAGCCCTTACCCATACATTTGGCTCAG 3720
Db 3661 TCCAGAAAGAGGCTTAGCAGAGATCTAGCCCTTACCCATACATTTGGCTCAG 3720
QY 3721 GTTACGGAAGAGGGGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780
Db 3721 GTTACGGAAGAGGGGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTTATTTGTAAGTAACAATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTTATTTGTAAGTAACAATATACCTTCTCAGT 3840
QY 3841 CTACTAGGCAATGACACGTTGCTACCGAGTGTCTGTAAAGCAACAAGAGAAATTTAT 3900
Db 3841 CTACTAGGCAATGACACGTTGCTACCGAGTGTCTGTAAAGCAACAAGAGAAATTTAT 3900
QY 3901 TATCATTTGAAGAAATAGCTTAATAGTACAGTAACAGTAATATTTGGCAAGCATCTC 3960
Db 3901 TATCATTTGAAGAAATAGCTTAATAGTACAGTAACAGTAATATTTGGCAAGCATCTC 3960
QY 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTTGTCTTCAAGTGA 4020
Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGCTAGCTTGTCTTCAAGTGA 4020
QY 4021 GTGAATTGGAAGCTTGAAGTGAACAAACCAAGATCCTTTCTTGAATTTGTTCTT 4080
Db 4021 GTGAATTGGAAGCTTGAAGTGAACAAACCAAGATCCTTTCTTGAATTTGTTCTT 4080
QY 4081 CCAAAACAATGAGGCACTAGTCTGAAGCCAGGAGTGTGCTGATGACAAAGATTTGG 4140
Db 4081 CCAAAACAATGAGGCACTAGTCTGAAGCCAGGAGTGTGCTGATGACAAAGATTTGG 4140
QY 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAATAATCAAGAAAGCAAGCA 4200
Db 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAATAATCAAGAAAGCAAGCA 4200
QY 4201 TGGATTCAAACTTAAGGGAAGCAGCATCTGGGTGTGAGTGAACAAGGCTCTGAG 4260
Db 4201 TGGATTCAAACTTAAGGGAAGCAGCATCTGGGTGTGAGTGAACAAGGCTCTGAG 4260
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGATACCATG 4320
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGATACCATG 4320
QY 4321 AACTATTAAGCTTAAGGCTCAGAGAGAAATGGCTGAATGAAGCTGTGTTGAACAGC 4380
Db 4321 AACTATTAAGCTTAAGGCTCAGAGAGAAATGGCTGAATGAAGCTGTGTTGAACAGC 4380
QY 4381 AACTATTAAGCTTAAGGCTCAGAGAGAAATGGCTGAATGAAGCTGTGTTGAACAGC 4440
Db 4381 AACTATTAAGCTTAAGGCTCAGAGAGAAATGGCTGAATGAAGCTGTGTTGAACAGC 4440

QY 4441 ACCGGAATTCAGAACCAAGCAGATCAGAAAAGCACTATTTAACTTCAGAGAAAGTA 4500
Db 4441 ACCGGAATTCAGAACCAAGCAGATCAGAAAAGCACTATTTAACTTCAGAGAAAGTA 4500
QY 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGTCTG 4560
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGTCTG 4560
QY 4561 CAGATAGTTCTACAGTAATAAATAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620
Db 4561 CAGATAGTTCTACAGTAATAAATAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620
QY 4621 GCCCATCATTAAGATGATAGTGTATGATGATGATGATGATGATGATGATGATGATG 4680
Db 4621 GCCCATCATTAAGATGATAGTGTATGATGATGATGATGATGATGATGATGATGATG 4680
QY 4681 ACTACCATCTCAGAGGAGCTCATTAAGTGTGATGATGATGATGATGATGATGATG 4740
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QY 4741 AGTCTGGGCAACAGATTTGAGGAAACATCTTACCTGCAAGGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCAACAGATTTGAGGAAACATCTTACCTGCAAGGCAAGATCTAGAGGAA 4800
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGATGATGATGATGATGATGATG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGATGATGATGATGATGATGATG 4860
QY 4861 AAGACAGAGCCCAAGAGTACGCTGTGTTGGCAATACATCTTCAACTCTGATTTGA 4920
Db 4861 AAGACAGAGCCCAAGAGTACGCTGTGTTGGCAATACATCTTCAACTCTGATTTGA 4920
QY 4921 AAGTCCCAATTTGAAAGTTGAGAGATCGCCAGAGTCAAGTGTGCTCATACACTG 4980
Db 4921 AAGTCCCAATTTGAAAGTTGAGAGATCGCCAGAGTCAAGTGTGCTCATACACTG 4980
QY 4981 ATACTGCTGGATATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAAACAGAAATGAC 5040
Db 4981 ATACTGCTGGATATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAAACAGAAATGAC 5040
QY 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGCTGAGCCTGACCCGAG 5100
Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGTGTGTGCTGAGCCTGACCCGAG 5100
QY 5101 AATTTATGCTGATGATCAAGTTTGCAGAAACACCAATCACTTAATCTTAATTA 5160
Db 5101 AATTTATGCTGATGATCAAGTTTGCAGAAACACCAATCACTTAATCTTAATTA 5160
QY 5161 CTGAAGAGACTCATGATGTTTATGAAGAAACAGATGCTGAGTTGTGTGAACGAGAC 5220
Db 5161 CTGAAGAGACTCATGATGTTTATGAAGAAACAGATGCTGAGTTGTGTGAACGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGGTATTTGCTGAGTGAACCC 5280
Db 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGGTATTTGCTGAGTGAACCC 5280
QY 5281 AGCTATTAAAGAAAGAAATGCTGAATGAGATGATTTTGAAGCAGAGGATGTGG 5340
Db 5281 AGCTATTAAAGAAAGAAATGCTGAATGAGATGATTTTGAAGCAGAGGATGTGG 5340
QY 5341 TCAATGGAAGAAACCAAGGTCAGAAAGCAGAGCAAGAGATCCAGAGAGAGATCT 5400
Db 5341 TCAATGGAAGAAACCAAGGTCAGAAAGCAGAGCAAGAGATCCAGAGAGAGATCT 5400
QY 5401 TCAAGGGGCTAAGATCTGTCTATGAGGCTTCAACCAATGCTGCTCAAGATCACTGG 5460
Db 5401 TCAAGGGGCTAAGATCTGTCTATGAGGCTTCAACCAATGCTGCTCAAGATCACTGG 5460

QY	1081	GGGCTGGAGTAAAGAAACATGTAATGATAGCGGACCTCCAGCACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAGTAAAGAAACATGTAATGATAGCGGACCTCCAGCACAGAAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGACAGAAACCTGCCATCT	1200
Db	1141	ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGACAGAAACCTGCCATCT	1200
QY	1201	CAGAGATCTCTAGAGATACCTGAAGATGTTCTTTGGATTAACACTAAATAGCAGATTCAGA	1260
Db	1201	CAGAGATCTCTAGAGATACCTGAAGATGTTCTTTGGATTAACACTAAATAGCAGATTCAGA	1260
QY	1261	AAGTTAATAGTGTGTTTCCAGAGATGATGAACCTGTAGGTTCTGATGACTCACATGATG	1320
Db	1261	AAGTTAATAGTGTGTTTCCAGAGATGATGAACCTGTAGGTTCTGATGACTCACATGATG	1320
QY	1321	GGGAGCTGGAATCCAAATGCGAAGTACGTAGTATGGAAGCTTCTTAATAGAGTATG	1380
Db	1321	GGGAGCTGGAATCCAAATGCGAAGTACGTAGTATGGAAGCTTCTTAATAGAGTATG	1380
QY	1381	AATATTCTGGTCTTTCAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTTAA	1440
Db	1381	AATATTCTGGTCTTTCAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTTAA	1440
QY	1441	TATGTAAAGTGAAGAGGTTCACTCCCAATCGTAAAGATATATTAAGAACAATAT	1500
Db	1441	TATGTAAAGTGAAGAGGTTCACTCCCAATCGTAAAGATATATTAAGAACAATAT	1500
QY	1501	TTGGGAAAACCTATGGAAGAAAGGCAAGCCTCCCACTTAAAGCAATTAATCTGAAAATC	1560
Db	1501	TTGGGAAAACCTATGGAAGAAAGGCAAGCCTCCCACTTAAAGCAATTAATCTGAAAATC	1560
QY	1561	TAATTATAGAGACATTTGTTACTGAGCCACAGATATATCAAGAGCGTCCCTCAATA	1620
Db	1561	TAATTATAGAGACATTTGTTACTGAGCCACAGATATATCAAGAGCGTCCCTCAATA	1620
QY	1621	AATTAAAGCTTAAAGAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG	1680
Db	1621	AATTAAAGCTTAAAGAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG	1680
QY	1681	CAGATTTGGCACTTCAAAAAGATCCCTGAATATATTAATCAGGAACTTAAACCAAGGAGC	1740
Db	1681	CAGATTTGGCACTTCAAAAAGATCCCTGAATATATTAATCAGGAACTTAAACCAAGGAGC	1740
QY	1741	AGAAATGCTCAATGTAATATTACTTAATAGTGTGATGAGAAATTAACCAAAAGGTGTT	1800
Db	1741	AGAAATGCTCAATGTAATATTACTTAATAGTGTGATGAGAAATTAACCAAAAGGTGTT	1800
QY	1801	CTATTCAAGATAGAAAAATCTCTAACCCATAGAACTACCTGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTCAAGATAGAAAAATCTCTAACCCATAGAACTACCTGAAAAAGAAATCTGCTTTCA	1860
QY	1861	AAACGAAGCTGACCTTAATACACACAGTATTAAGCAATATGGAATCTGAAATTAATATCC	1920
Db	1861	AAACGAAGCTGACCTTAATACACACAGTATTAAGCAATATGGAATCTGAAATTAATATCC	1920
QY	1921	ACAATTCAAAAGCACCTTAAAAAGATTAAGGCTGAGAGAGAGTCTTCTACAGGCATATTC	1980
Db	1921	ACAATTCAAAAGCACCTTAAAAAGATTAAGGCTGAGAGAGAGTCTTCTACAGGCATATTC	1980
QY	1981	ATGCGCTTGAACTAGTAGTCACTAGTAAATCTTAAAGCCCACTTAATTTGATCTGAATTGCAA	2040
Db	1981	ATGCGCTTGAACTAGTAGTCACTAGTAAATCTTAAAGCCCACTTAATTTGATCTGAATTGCAA	2040
QY	2041	TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAGTACAACTAAATGGCAGTCA	2100
Db	2041	TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAGTACAACTAAATGGCAGTCA	2100
QY	2101	GGCAGAGAGAAACCTACACTCATGGAAGGTAAAGAACTGCAACTGGACCCAAAGAGA	2160
Db	2101	GGCAGAGAGAGAAACCTACACTCATGGAAGGTAAAGAACTGCAACTGGACCCAAAGAGA	2160
QY	2161	GTAAACAGCAATATGAACAGACAACTAAAGAATGATGACAGGATATCTTTCCAGAGCTGA	2220

Db	2161	GTAAACAAGCCAATATGACAGACAAAGTAAACATGACAGGAATCTTTCCACAGCTGA	2220
Qy	2221	AGTTAAACAAATGACACCTGGTCTTTTAACTAGTGTCAAAATACCAAGTCACTTAAAGAT	2280
Db	2221	AGTTAAACAATGACACCTGGTCTTTTAACTAGTGTCAAAATACCAAGTCACTTAAAGAT	2280
Qy	2281	TTGTCAATCTAGCCCTTCCAAAGAGAAAAAGAGAAAACTAGAAAACGTTAAAGTG	2340
Db	2281	TTGTCAATCTAGCCCTTCCAAAGAGAAAAAGAGAAAACTAGAAAACGTTAAAGTG	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGGAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGGAACTG	2400
Qy	2401	AAAGATCTGTAAGAGTAGAGTAGAGTATTTATGTTGTAACCTGGTACTGATTTAAGGCACTAGG	2460
Db	2401	AAAGATCTGTAAGAGTAGAGTAGAGTATTTATGTTGTAACCTGGTACTGATTTAAGGCACTAGG	2460
Qy	2461	AAAGTATCTGTTACTGTGAGTAGTACCTAGGGAAGGCAAAAAAGAACTCAATTAAT	2520
Db	2461	AAAGTATCTGTTACTGTGAGTAGTACCTAGGGAAGGCAAAAAAGAACTCAATTAAT	2520
Qy	2521	GTTGAGTCAAGTGTGACGATTTTGAACCCCAAGGGACTAATCATGTTGTTCCAAAG	2580
Db	2521	GTTGAGTCAAGTGTGACGATTTTGAACCCCAAGGGACTAATCATGTTGTTCCAAAG	2580
Qy	2581	ATPAATAGAAATGACACAGAAAGGCTTTAAGTATCAATGGGACATGAAGTTAACACAGTC	2640
Db	2581	ATPAATAGAAATGACACAGAAAGGCTTTAAGTATCAATGGGACATGAAGTTAACACAGTC	2640
Qy	2641	GGGAAACAAGCATAGAAAAATGGAAGAAAGTAACCTTAGTGTCTCAATTTTGCAGATATCAT	2700
Db	2641	GGGAAACAAGCATAGAAAAATGGAAGAAAGTAACCTTAGTGTCTCAATTTTGCAGATATCAT	2700
Qy	2701	TCAAGCTTTCAAAGGCCAGTCAATTTGTCTGTTTCAATCCAGGAATGACAGAAAGG	2760
Db	2701	TCAAGCTTTCAAAGGCCAGTCAATTTGTCTGTTTCAATCCAGGAATGACAGAAAGG	2760
Qy	2761	AATGGAACAATCTCTGCGCACTCTGGGATCCTTAAAGAAACAAGTCCAAAGTCACTT	2820
Db	2761	AATGGAACAATCTCTGCGCACTCTGGGATCCTTAAAGAAACAAGTCCAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGGAGAAAAATCAGGAAAAAGATGAGTCTAATATCAAGCTGTAC	2880
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Db	2881	AGACAGTTAATATCACTGACAGGCTTTCTGTGTGTTGTCAGAAAGATTAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGATATCAAAAGAGGCTTGGTTTGTCTATCATCTCAAGTTCAAGGCA	3000
Db	2941	ATGCCAAATGATATCAAAAGAGGCTTGGTTTGTCTATCATCTCAAGTTCAAGGCA	3000
Qy	3001	ACGAACCTGAGCTACTTACTCCAATTAACAATGACACTTTTACAAAACCATATCTGATAC	3060
Db	3001	ACGAACCTGAGCTACTTACTCCAATTAACAATGACACTTTTACAAAACCATATCTGATAC	3060
Qy	3061	CACCACTTTTCCATCAAGTCAATTTGTAAACCTAATGTAAAGAAAAATCTCTAGAGG	3120
Db	3061	CACCACTTTTCCATCAAGTCAATTTGTAAACCTAATGTAAAGAAAAATCTCTAGAGG	3120
Qy	3121	AAAACCTTGAGGAACATTCAATGTCACCTGAAGAGAAATGGGAAATGAGAACATTTCCAA	3180
Db	3121	AAAACCTTGAGGAACATTCAATGTCACCTGAAGAGAAATGGGAAATGAGAACATTTCCAA	3180
Qy	3181	GTACAGTAGACAAATTAGCCGTATTAACAATTAGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
Db	3181	GTACAGTAGACAAATTAGCCGTATTAACAATTAGAGAAAAATGTTTTTAAAGAACCAAGCT	3240
Qy	3241	CAGCAATATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA	3300
Db	3241	CAGCAATATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA	3300

AAZ87995
ID AAZ87995 standard; DNA: 5712 BP.
XX
AC AAZ87995;
XX
DT 06-JUN-2000 (first entry)
XX
DE BRCA1 gene sequence (GenBank Accn No: U14680).
XX
KW BRCA1; tumour; prostate cancer; cytostatic; antiproliferative;
XX gene therapy; ds.
XX
OS Homo sapiens.
XX
FH
FH Key Location/Qualifiers
FT CDS
FT 120..5711
FT /*tag= a
FT /transl_except= (pos: 1452..1454, aa:Asp)
FT /transl_except= (pos: 1482..1484, aa:Asp)
FT /transl_except= (pos: 1581..1583, aa:Ser)
FT /transl_except= (pos: 1899..1901, aa:Glu)
FT /transl_except= (pos: 1902..1904, aa:Leu)
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FT /transl_except= (pos: 4533..4535, aa:Xaa)
FT /transl_except= (pos: 4689..4691, aa:Pro)
FT /note= "Xaa= unknown"
XX
XX CA218197-A1.
XX
PD 05-JUN-1999.
XX
XX 12-DEC-1997; 97CA-2218197.
XX
XX 05-DEC-1997; 97US-0986106.
XX
XX (UNIM) UNIV WASHINGTON.
XX (UYVA-) UNIV VANDERBILT.
XX
XX Robinson-Benion CL, Thompson ME, Holt JT, Jensen RA, Steiner MS;
XX King M;
XX MPI; 2000-238071/21.
XX P-PSDB; AAY77818.
XX
XX New method of treatment and suppression of prostate cancer comprises
XX using the BRCA family of genes to decrease the growth rate of the tumor
XX
XX Claim 11; Page 98-104; 166pp; English.
XX
XX The invention relates to a method for suppressing the growth of a
XX prostate tumour in a mammal that comprises introducing to the tumour a
XX vector comprising a nucleic acid sequence encoding a BRCA family gene
XX product operatively linked to a promoter, where production of the BRCA
XX family gene product results in a decrease in the growth rate of the
XX tumour. The methods are used to suppress the growth of and also to treat
XX prostate tumour in a mammal where the tumour is gene-linked hereditary
XX prostate cancer or sporadic prostate cancer. The present sequence
XX represents a BRCA1 gene sequence (GenBank Accn No: U14680) that can be
XX administered for suppressing tumour.
XX
XX Sequence 5712 BP; 1956 A; 1099 C; 1274 G; 1383 T; 0 other;
XX
XX Query Match 100.0%; Score 5709.4; DB 21; Length 5712;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCCTGAGACCCCGACACAGGCTGTGGGGTTTCTCAGATAACTGGGGC 60
DB 1 AGCTGCTGAGACTTCCTGAGACCCCGACACAGGCTGTGGGGTTTCTCAGATAACTGGGGC 60
QY 61 CCTGGGCTCAGAGAGGCTTCACTCTCTGCTGTGGTAAAGTTCATTGGAACAGAAAGAA 120
DB 61 CCTGGGCTCAGAGAGGCTTCACTCTCTGCTGTGGTAAAGTTCATTGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTGGCGTTGAGAGAGTCAAAATGTCAATTAATGCTATGACAGAAA 180
DB 121 TGGATTATCTGCTCTTGGCGTTGAGAGAGTCAAAATGTCAATTAATGCTATGACAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTCATCAAGAACCTGTCCCAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTTCATCAAGAACCTGTCCCAAGTGTGACC 240
QY 241 ACATATTTTGGCAAAATTTTGGCATGTGAAACTTCTCAACAGAGAAAGGGCTTCACT 300
DB 241 ACATATTTTGGCAAAATTTTGGCATGTGAAACTTCTCAACAGAGAAAGGGCTTCACT 300
QY 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCCTACAGAAAGTACGAGATTAGTC 360
DB 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCCTACAGAAAGTACGAGATTAGTC 360
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DB 361 AACTGTTGAAGAGCTATTTGAATATCATTTGTGCTTTGAGTTCAGCTTGACAGGTTGAGT 420
QY 421 ATGCAAAACAGCTATATTTTGGCAAAAGAGAAATTAATCTCTCTGAACTCTTAAAGATG 480
DB 421 ATGCAAAACAGCTATATTTTGGCAAAAGAGAAATTAATCTCTCTGAACTCTTAAAGATG 480
QY 481 AAGTTTCTATCTCCAAAGTATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCTCCAAAGTATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540
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 PR 20-FEB-1996; 96US-0603753.
 XX
 PA (UNIVV-) UNIV VANDERBILT.
 XX (UNIV) UNIV WASHINGTON.
 PI
 PI Claire-King M, Holt JT, Jensen RA, Jettison TL, Page DL;
 PI Robinson-Benton CL, Szabo CI, Thompson ME;
 DR WPI: 1997-434733/40.
 DR P-PSDB: AAW23286.
 PS
 PS Claim 13; Page 54-63; 148bp: English.
 CC This sequence comprises a full-length BRCA1 cDNA. Genetic analysis
 CC of familial and ovarian cancer indicates that BRCA1 is a tumour
 CC suppressor gene. It encodes a 190 kDa protein (see AAW23286) that is
 CC an inhibitor of the growth and proliferation of human breast and
 CC ovarian cancer cells. DNA encoding the BRCA1 protein can thus be
 CC used in gene therapy methods for the treatment of breast and
 CC ovarian cancers. A purified BRCA1 protein can also be used to treat
 CC these cancers and, since it is secreted, can be used to identify
 CC the BRCA1 receptor and hence to identify BRCA1 protein-mimetic
 CC agents which act on the receptor for use in breast and ovarian
 CC cancer treatment. The BRCA2 gene (see AAT84841) and BRCA2 protein
 CC (see AAW2287) have also been characterized. Methods are claimed for
 CC the isolation of BRCA1 or BRCA2 receptors, and for treating or
 CC preventing breast and (gene-linked hereditary or sporadic) ovarian
 CC cancers using BRCA1 and BRCA2 proteins and genes.
 XX
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 Query Match 100.0%; Score 5709.4; DB 18; Length 5712;
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Qy 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAAATGGTACTTACTATTTCTGGGTGACC 5280
Db 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAAATGGTACTTACTATTTCTGGGTGACC 5280
Qy 5281 AGCTATTTAAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGGG 5340
Db 5281 AGCTATTTAAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGGG 5340
Qy 5341 TCAATGGAAGAAACCAACAGGTCACAAAGCAGAGAAATCCAGACAGAAAGATCT 5400
Db 5341 TCAATGGAAGAAACCAACAGGTCACAAAGCAGAGAAATCCAGACAGAAAGATCT 5400
Qy 5401 TCAGGGGGCTAGAAATCTGTTCTATGAGCCTTCAACCAATGCCCAAGATCAACTGG 5460
Db 5401 TCAGGGGGCTAGAAATCTGTTCTATGAGCCTTCAACCAATGCCCAAGATCAACTGG 5460
Qy 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520
Qy 5521 GCACAGGTGTCACCAATTTGTTGTTGTCACAGACCTGAGATCCTGACAGAGACAAATGCT 5580
Db 5521 GCACAGGTGTCACCAATTTGTTGTTGTCACAGACCTGAGATCCTGAGACAGAGACAAATGCT 5580
Qy 5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
Db 5581 TCCATGCAATTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 5640
Qy 5641 GTGTGACACTTACAGAGTCCAGAGCTGAGACACCTGATGATGATGATGATGATGATG 5700
Db 5641 GTGTGACACTTACAGAGTCCAGAGCTGAGACACCTGATGATGATGATGATGATGATG 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 11
AAT8480
ID AAT8480 strand: cDNA to mRNA; 5712 BP.
XX
AC AAT8480;
XX
DT 21-FEB-1998 (first entry)
XX
DE Human breast and ovarian cancer susceptibility gene BRCA1.
XX
KW BRCA1; breast cancer; ovarian cancer; human;
XX tumour suppressor gene; gene therapy; receptor; ds.
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT 120..5711
FT /tag= a
FT /transl_except= (pos:1482..1484, aa:Asp)
FT /transl_except= (pos:1581..1583, aa:Ser)
FT /transl_except= (pos:1899..1901, aa:Glu)
FT /transl_except= (pos:1902..1904, aa:Leu)
FT /transl_except= (pos:1905..1907, aa:Glu)
FT /transl_except= (pos:1908..1910, aa:Leu)
FT /transl_except= (pos:1911..1913, aa:Asn)
FT /transl_except= (pos:1914..1916, aa:Ile)

```


QY 1801 CTATTGAGATGAGAAAAATCTTAACCCAAATAGAACTACTCGAAAAAGAAATCTGCTTTCA 1860
 Db 1801 CTATTGAGATGAGAAAAATCTTAACCCAAATAGAACTACTCGAAAAAGAAATCTGCTTTCA 1860
 QY 1861 AAACGAAAGCTGAACTTAAGACAGACATTAAGCAATATGGAATCTCGAAATTAATATCC 1920
 Db 1861 AAACGAAAGCTGAACTTAAGACAGACATTAAGCAATATGGAATCTCGAAATTAATATCC 1920
 QY 1921 ACAATTCAAAAGCACCTTAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
 Db 1921 ACAATTCAAAAGCACCTTAAGAAATAGGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980
 QY 1981 ATGGCTTGAACCTAGTAGCAAGAAATCTAAGCCCACTAATTTGTAATGCAAA 2040
 Db 1981 ATGGCTTGAACCTAGTAGCAAGAAATCTAAGCCCACTAATTTGTAATGCAAA 2040
 QY 2041 TTGATAGTGTCTCTGAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2100
 Db 2041 TTGATAGTGTCTCTGAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCCAGTCA 2100
 QY 2101 GGACAGCAGAAAACTTACAACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
 Db 2101 GGACAGCAGAAAACTTACAACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160
 QY 2161 GTAAACAGCCAAATGAAAGACAGCAATGAAAGACATGACAGCATCTTTCCAGAGCTGA 2220
 Db 2161 GTAAACAGCCAAATGAAAGACAGCAATGAAAGACATGACAGCATCTTTCCAGAGCTGA 2220
 QY 2221 AGTTAACAAATGCACTGCTTTTCTTAAGTGTTCAAATACCAAGTAAAGTAAAGT 2280
 Db 2221 AGTTAACAAATGCACTGCTTTTCTTAAGTGTTCAAATACCAAGTAAAGTAAAGT 2280
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 Db 2281 TTGTCATCTCTAGCCTTCCAAAGAGAAAAAGAGAGAACTAGAAACAGTTAAAGT 2340
 QY 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400
 Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400
 QY 2401 AAAATCTGTAGAGATGACATTTTCAATGCTGCTGATCTGATTTAGGCACTCAGG 2460
 Db 2401 AAAATCTGTAGAGATGACATTTTCAATGCTGCTGATCTGATTTAGGCACTCAGG 2460
 QY 2461 AAAATCTGTAGAGATGACATTTTCAATGCTGCTGATCTGATTTAGGCACTCAGG 2520
 Db 2461 AAAATCTGTAGAGATGACATTTTCAATGCTGCTGATCTGATTTAGGCACTCAGG 2520
 QY 2521 GTGTGAGTCACTGTGACAGATTTTGAAGACCCCAAGGACATTAATGATGTTTCCAAAG 2580
 Db 2521 GTGTGAGTCACTGTGACAGATTTTGAAGACCCCAAGGACATTAATGATGTTTCCAAAG 2580
 QY 2581 ATATATAGAAATGACACAGAGAGCTTTAATGATCTGATGAGACATGAATTAACCAAGT 2640
 Db 2581 ATATATAGAAATGACACAGAGAGCTTTAATGATCTGATGAGACATGAATTAACCAAGT 2640
 QY 2641 GGGAAACAGCATGAAATGAGAAATGAACTTGAATGCTCAGATTTTGAAGATTAAT 2700
 Db 2641 GGGAAACAGCATGAAATGAGAAATGAACTTGAATGCTCAGATTTTGAAGATTAAT 2700
 QY 2701 TCAAGGTTTCAAGAGCCAGTCAATTTGCTGCTGTTTCAATTCAGAAATGAGAAAGG 2760
 Db 2701 TCAAGGTTTCAAGAGCCAGTCAATTTGCTGCTGTTTCAATTCAGAAATGAGAAAGG 2760
 QY 2761 AATGTGCAACATTTCTGCTCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820
 Db 2761 AATGTGCAACATTTCTGCTCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820
 QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGGCTGTAC 2880
 Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAAGATGAGTCTAATATCAAGGCTGTAC 2880

QY 2881 AGACAGTTAATATCACTGACAGGCTTTCTGTGTTGTGACGAAAGATTAAGCCAGTTGATA 2940
 Db 2881 AGACAGTTAATATCACTGACAGGCTTTCTGTGTTGTGACGAAAGATTAAGCCAGTTGATA 2940
 QY 2941 ATGCCAAATGTATGATCAAGAGGCTCTAGCTTTTGTATCATCTCAGTCAAGAGCA 3000
 Db 2941 ATGCCAAATGTATGATCAAGAGGCTCTAGCTTTTGTATCATCTCAGTCAAGAGCA 3000
 QY 3001 ACGAAATCTGACCTATCTCAATTAACATGACATTTTAAACAAACCCATATCTGTATAC 3060
 Db 3001 ACGAAATCTGACCTATCTCAATTAACATGACATTTTAAACAAACCCATATCTGTATAC 3060
 QY 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACTAATGTAGAAAAATCTGCTAGAG 3120
 Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACTAATGTAGAAAAATCTGCTAGAG 3120
 QY 3121 AAACTTTGAGAAACATTCATGTCACCTGAAAGAAATGAGAAATGAGAAACATTCGCA 3180
 Db 3121 AAACTTTGAGAAACATTCATGTCACCTGAAAGAAATGAGAAATGAGAAACATTCGCA 3180
 QY 3181 GTACAGTGAAGACAAATTAGCCGTATTAACATTAAGAAATGTTTAAAGAAAGCCAGT 3240
 Db 3181 GTACAGTGAAGACAAATTAGCCGTATTAACATTAAGAAATGTTTAAAGAAAGCCAGT 3240
 QY 3241 CAAGCAATATTAATGAAGTATGCTTCCAGTACTAATGAAGTGGCTCCAGTATTAAGAA 3300
 Db 3241 CAAGCAATATTAATGAAGTATGCTTCCAGTACTAATGAAGTGGCTCCAGTATTAAGAA 3300
 QY 3301 TAGGTTCCAGTATGAAACATTTAGACAGAACTAGGTAGAAACAGAGGCCCAAAATTTGA 3360
 Db 3301 TAGGTTCCAGTATGAAACATTTAGACAGAACTAGGTAGAAACAGAGGCCCAAAATTTGA 3360
 QY 3361 ATGCTATGCTTGAATGAGGTTTTCGACACCTGAGCTGTAAACAAAGCTTCTCGGAA 3420
 Db 3361 ATGCTATGCTTGAATGAGGTTTTCGACACCTGAGCTGTAAACAAAGCTTCTCGGAA 3420
 QY 3421 GTAAATGTAGCATCTGAAATTAAGAAAGAAAGATTAAGAAAGTTCAGACTGTTA 3480
 Db 3421 GTAAATGTAGCATCTGAAATTAAGAAAGAAAGATTAAGAAAGTTCAGACTGTTA 3480
 QY 3481 ATACAGATTTTCTCCATATCTGATTTCAATTAATTAAGAAACAGCTTATGGAAGTATG 3540
 Db 3481 ATACAGATTTTCTCCATATCTGATTTCAATTAATTAAGAAACAGCTTATGGAAGTATG 3540
 QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGTAATTAAGG 3600
 Db 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGTAATTAAGG 3600
 QY 3601 AAGATCTAGTTTGTCTGAAATTAAGCAATTAAGAAAGTTCGCTGTTTTCGCAAAAGG 3660
 Db 3601 AAGATCTAGTTTGTCTGAAATTAAGCAATTAAGAAAGTTCGCTGTTTTCGCAAAAGG 3660
 QY 3661 TTCAGAAAGAGAGCTTATGACAGAGTCTAGCCCTTTACCCATACACATTTGCTCAGG 3720
 Db 3661 TTCAGAAAGAGAGCTTATGACAGAGTCTAGCCCTTTACCCATACACATTTGCTCAGG 3720
 QY 3721 GTTACGAGAGAGGAGCAAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGGAGAGG 3780
 Db 3721 GTTACGAGAGAGGAGCAAGAAATTAAGAGTCTCAGAGAGAACTTATCTAGGAGAGG 3780
 QY 3781 AAGAGCTTCCCTGTTCCAACTGTTATTTTGTAAAGTAAACAAATATACCTTCTCAGT 3840
 Db 3781 AAGAGCTTCCCTGTTCCAACTGTTATTTTGTAAAGTAAACAAATATACCTTCTCAGT 3840
 QY 3841 CTACTAGGATAGACCGTTGCTTACCGAGTGTCTGTAAAGCAACAGAGGAGAAATTTAT 3900
 Db 3841 CTACTAGGATAGACCGTTGCTTACCGAGTGTCTGTAAAGCAACAGAGGAGAAATTTAT 3900
 QY 3901 TATCATTAAGAAATATAGCTTAATGATGACGATACCAAGGATTAATTTGCAAGGACATTC 3960
 Db 3901 TATCATTAAGAAATATAGCTTAATGATGACGATACCAAGGATTAATTTGCAAGGACATTC 3960
 QY 3961 AGGAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTTGTCTTCTCAAGTGA 4020

PT BRCA1 omi gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer

XX Claim 2e; Page -; 54dp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi2 gene in which a polymorphic variation occurs at
CC nucleotide 3687. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi2 gene represented in AAV46449.

XX Sequence 5711 BP, 1955 A, 1098 C, 1274 G, 1383 T, 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGTGAGACTTCTTGAGACCCCGACACGCGTGTGGGTTTCATGATACTGAGCC 60
DB 1 AGCTCGTGAGACTTCTTGAGACCCCGACACGCGTGTGGGTTTCATGATACTGAGCC 60
QY 61 CCTGGCGTGAAGAGGCGCTTACCCCTGCTCTGCTGAGTAAGTCAATGATGGAACAGAAAGAA 120
DB 61 CCTGGCGTGAAGAGGCGCTTACCCCTGCTCTGCTGAGTAAGTCAATGATGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTCCGCTGGAAGAGTAAGTAATGCTAATGCTATGACAGAAA 180
DB 121 TGGATTATCTGCTCTTCCGCTGGAAGAGTAAGTAATGCTAATGCTATGACAGAAA 180
QY 181 TCTTTAAGTGTCCCATCTGCTGCTGAGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC 240
DB 181 TCTTTAAGTGTCCCATCTGCTGCTGAGAGTTGATCAAGAACTGTCTCCACAAAGTGTGACC 240
QY 241 ACATATTTGCAAAATTTGATGCTGAACTTCTCAACGAGAAAGGCGCTTCAAGT 300
DB 241 ACATATTTGCAAAATTTGATGCTGAACTTCTCAACGAGAAAGGCGCTTCAAGT 300
QY 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCCTACAAAGAAAGTACAGATTAGTC 360
DB 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCCTACAAAGAAAGTACAGATTAGTC 360
QY 361 AACTTGTGAAGGCTATGTAATAATCATTTGCTTTTACGCTTGACACAGGTTTGAAGT 420
DB 361 AACTTGTGAAGGCTATGTAATAATCATTTGCTTTTACGCTTGACACAGGTTTGAAGT 420
QY 421 ATGCAAAAGAGCTAATTTTGAAGAAAGAAATTAATCTCTGGAACATCTAAGAGATG 480
DB 421 ATGCAAAAGAGCTAATTTTGAAGAAAGAAATTAATCTCTGGAACATCTAAGAGATG 480
QY 481 AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTCCAAAAGCTTCTACAGATG 540
DB 481 AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTCCAAAAGCTTCTACAGATG 540
QY 541 AACCCGAAATCTCTTCTTGAGAGAAACAGCTCTCACTGCTCAACTCTTCAAGCTTGA 600
DB 541 AACCCGAAATCTCTTCTTGAGAGAAACAGCTCTCACTGCTCAACTCTTCAAGCTTGA 600
QY 601 CTGTGGAACCTTGAGAGCAAGAGGAGATACCACTCAAAAGAGCTGTCTACATG 660
DB 601 CTGTGGAACCTTGAGAGCAAGAGGAGATACCACTCAAAAGAGCTGTCTACATG 660
QY 661 AATTGGATCTGATCTTCTGGAAGATACGTTAATAAGCACTTATGCAAGTGTGGAG 720
DB 661 AATTGGATCTGATCTTCTGGAAGATACGTTAATAAGCACTTATGCAAGTGTGGAG 720

DB 661 AATTGGATCTGATCTTCTGGAAGATACGTTAATAAGCACTTATGCAAGTGTGGAG 720
QY 721 ATCAAGAAATTTGTACAAATCACCCTCAAGAAACAGGATGAATCACTTTGATTCG 780
DB 721 ATCAAGAAATTTGTACAAATCACCCTCAAGAAACAGGATGAATCACTTTGATTCG 780
QY 781 CAAAAAGGCTCTGTGTAATTTTCTGAGACGATGTAACTAATCAATCAATCATCAAC 840
DB 781 CAAAAAGGCTCTGTGTAATTTTCTGAGACGATGTAACTAATCAATCAATCATCAAC 840
QY 841 CCAAGTAATATGATTTGAACACACCTAGAGAGCGTACAGAGGATCCAGAAAGT 900
DB 841 CCAAGTAATATGATTTGAACACACCTAGAGAGCGTACAGAGGATCCAGAAAGT 900
QY 901 ATCAGGATGTTCTGTTTAACTTGCATGTGAGAGCATGTGGCAATATCTCATGCCA 960
DB 901 ATCAGGATGTTCTGTTTAACTTGCATGTGAGAGCATGTGGCAATATCTCATGCCA 960
QY 961 GCTCATTTACAGATGAGAACACAGCTTTTACTCACTAAACAGAAATGATGAGAA 1020
DB 961 GCTCATTTACAGATGAGAACACAGCTTTTACTCACTAAACAGAAATGATGAGAA 1020
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTACAGAGGCCAATTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTACAGAGGCCAATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGATATGATAGGCGACTCCGACACAGAAAAAGTATG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGATATGATAGGCGACTCCGACACAGAAAAAGTATG 1140
QY 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGAATGAAGCAAAATGCTCATGCT 1200
DB 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGAATGAAGCAAAATGCTCATGCT 1200
QY 1201 CAGAGAACTCTAGAGATGAGAAATGTTCTTGATTAACCTAATATACAGATTCAGA 1260
DB 1201 CAGAGAACTCTAGAGATGAGAAATGTTCTTGATTAACCTAATATACAGATTCAGA 1260
QY 1261 AAGTTAATAGGTTTTCAGAAAGTAACTGTTAGTTCTGATGACTCAATGATG 1320
DB 1261 AAGTTAATAGGTTTTCAGAAAGTAACTGTTAGTTCTGATGACTCAATGATG 1320
QY 1321 GGAAGCTGAATCAAAATGCAAGTATGATGATTTGACGTTCTAATGAGTGTATG 1380
DB 1321 GGAAGCTGAATCAAAATGCAAGTATGATGATTTGACGTTCTAATGAGTGTATG 1380
QY 1381 AATATTCTGTTCTTCAAGAAATAGACTTACGCGCAGTATCCTCATGAGGCTTTAA 1440
DB 1381 AATATTCTGTTCTTCAAGAAATAGACTTACGCGCAGTATCCTCATGAGGCTTTAA 1440
QY 1441 TATGTAAAGTAAAGAGTCTCACTCAATTCAGTATGAGTAAATTTGAAGCAAAATAT 1500
DB 1441 TATGTAAAGTAAAGAGTCTCACTCAATTCAGTATGAGTAAATTTGAAGCAAAATAT 1500
QY 1501 TTGGGAAAACCTATCGAAGAGAGCAGCTCCCACTTAAGCCATGTAACGAAATC 1560
DB 1501 TTGGGAAAACCTATCGAAGAGAGCAGCTCCCACTTAAGCCATGTAACGAAATC 1560
QY 1561 TAAATTATAGGACATTTGTTACTGAGCCACAGATTAATACAGAGCTCCCTTCAAAATA 1620
DB 1561 TAAATTATAGGACATTTGTTACTGAGCCACAGATTAATACAGAGCTCCCTTCAAAATA 1620
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DB 1621 AATTAAGGCTAAAGAGACCTACATCGGCTTCACTGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTGGCACTTCAAAAGACTCTGGAATGATTAATCAGGAACTAACAACGAGAC 1740
DB 1681 CAGATTGGCACTTCAAAAGACTCTGGAATGATTAATCAGGAACTAACAACGAGAC 1740
QY 1741 AGAATGCTCAAGTATGATTAATTAATAGTGTATAGAAATTAACAAAGGTGATT 1800
DB 1741 AGAATGCTCAAGTATGATTAATTAATAGTGTATAGAAATTAACAAAGGTGATT 1800

QY	4201	TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGGTGGAGGTGAACAAAGCCCTCTGAG	4260
Db	4201	TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGGTGGAGGTGAACAAAGCCCTCTGAG	4260
QY	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGCATTTTAAACACTCAGCAGAGGGATACATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGCATTTTAAACACTCAGCAGAGGGATACATGC	4320
QY	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTAGAACACG	4380
Db	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTAGAACACG	4380
QY	4381	ATGGAGCCAGCCCTCTAACACTACCTACCTCCATATAGTACGCTTCTGCCCCGTGAG	4440
Db	4381	ATGGAGCCAGCCCTCTAACACTACCTACCTCCATATAGTACGCTTCTGCCCCGTGAG	4440
QY	4441	ACCTGCGAAATCCAGAACAAAGCAGATCGAAAAAGCAGTATTAACCTTCAAGAAAACTA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCAGATCGAAAAAGCAGTATTAACCTTCAAGAAAACTA	4500
QY	4501	GTGAATACCCCTTAAGCCCAAAATCCAGAAAGCCCTTCTGCTGACAAGTTTGAAGTGTG	4560
Db	4501	GTGAATACCCCTTAAGCCCAAAATCCAGAAAGCCCTTCTGCTGACAAGTTTGAAGTGTG	4560
QY	4561	CAGATAGTTCTACCGAGTAAAAATTAAGAACCGAGGTGAAGAAAGTCATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTACCGAGTAAAAATTAAGAACCGAGGTGAAGAAAGTCATCCCTCTTAAT	4620
QY	4621	GCCCATCATTTAGATGATAGTGTGATGCAATGCAAGTTGCTGGAGTCTTCAGAAATGAA	4680
Db	4621	GCCCATCATTTAGATGATAGTGTGATGCAATGCAAGTTGCTGGAGTCTTCAGAAATGAA	4680
QY	4681	ACTACCCATCTCAAGAGAGCTCATTAAGTTGTTGATGTGAGAGCAACGCTGAG	4740
Db	4681	ACTACCCATCTCAAGAGAGCTCATTAAGTTGTTGATGTGAGAGCAACGCTGAG	4740
QY	4741	AGTCGGGGCACAAGATTTGAAGGAAACATCTTATTCGCAAGCAAGCAATCTAAGGGAA	4800
Db	4741	AGTCGGGGCACAAGATTTGAAGGAAACATCTTATTCGCAAGCAAGCAATCTAAGGGAA	4800
QY	4801	CCCCCTTACCTGGAAATCTGGAAATCAGCCCTTCTCTGATGAGCCCTGAATCTGATCCTTG	4860
Db	4801	CCCCCTTACCTGGAAATCTGGAAATCAGCCCTTCTCTGATGAGCCCTGAATCTGATCCTTG	4860
QY	4861	AAAGCAGAGCCCCAGAGTCAAGTCTGTGTGGCACAATCAATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAAGCAGAGCCCCAGAGTCAAGTCTGTGTGGCACAATCAATCTTCAACCTCTGCATTTGA	4920
QY	4921	AAGTCCCCCAATGGAAGTGTGAGAAATCTGCCAGAGTCCAGCTGCTGCTATCTACTG	4980
Db	4921	AAGTCCCCCAATGGAAGTGTGAGAAATCTGCCAGAGTCCAGCTGCTGCTATCTACTG	4980
QY	4981	ATACTGCTGGGTATATATGCAATGCAAGAAAGTGTGAGCAGGGAGAACCAAAATTTGACAG	5040
Db	4981	ATACTGCTGGGTATATATGCAATGCAAGAAAGTGTGAGCAGGGAGAACCAAAATTTGACAG	5040
QY	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTGCTGAGCCCAAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTGCTGAGCCCAAG	5100
QY	5101	AATTTATCTGTGTGTCACAAAGTTTGGCAGAAAAACACCAATCACTTAATCTAATTA	5160
Db	5101	AATTTATCTGTGTGTCACAAAGTTTGGCAGAAAAACACCAATCACTTAATCTAATTA	5160
QY	5161	CTGAAGAGACTACTAGTGTGTTATGAAAACAGATGCTGAGTTTGTGTGAACGGAAC	5220
Db	5161	CTGAAGAGACTACTAGTGTGTTATGAAAACAGATGCTGAGTTTGTGTGAACGGAAC	5220
QY	5221	TGAATATATTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCATTTCTCGGGTGACC	5280
Db	5221	TGAATATATTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCATTTCTCGGGTGACC	5280
QY	5281	AGTCTATTTAAAGAAAAATGCTGGAATGACATGATTTTGAAGTCAAGAGAGATGTGG	5340

Db	5281	AGCTATTATTAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTGG	5340
Qy	5341	TCAAATGAGAAACACCAAGGTCACAAAGCAGACAGAGATCCACAGACAGAAAGATCT	5400
Db	5341	TCATATGAGAAACACCAAGGTCACAAAGGAGCAGACAGAGATCCACAGACAGAAAGATCT	5400
Qy	5401	TCAGGGGGCTTGAAGATCTGTTGCTATAGGGCCCTTCACCAACATGCCACAGATCACTGG	5460
Db	5401	TCAGGGGGCTTGAAGATCTGTTGCTATAGGGCCCTTCACCAACATGCCACAGATCACTGG	5460
Qy	5461	AATGGATGGTACACCTGTGTGGTCCCTGTGTGGTGAAGAGCTTCAATTCACCCCTTG	5520
Db	5461	AATGGATGGTACACCTGTGTGGTCCCTGTGTGGTGAAGAGCTTCAATTCACCCCTTG	5520
Qy	5521	GCACAGGTGTCACCAATTTGTGGTTGTGACGCAGATGCTGTGACAGAGACATGGCT	5580
Db	5521	GCAAGAGGTGTCACCAATTTGTGGTTGTGACGCAGATGCTGTGACAGAGACATGGCT	5580
Qy	5581	TCCATGCAATTTGGGCAGATGTTGAGGACACCTGTGTGTGACCCGAGAGTGGGTGTTGACA	5640
Db	5581	TCCATGCAATTTGGGCAGATGTTGAGGACACCTGTGTGTGACCCGAGAGTGGGTGTTGACA	5640
Qy	5641	GTGTAGCACTTACCAAGTGCACGAGAGCTGTGACACCTTACCTGATACCCCAATCCCCACA	5700
Db	5641	GTGTAGCACTTACCAAGTGCACGAGAGCTGTGACACCTTACCTGATACCCCAATCCCCACA	5700
Qy	5701	GGCACTACTGA	5711
Db	5701	GGCACTACTGA	5711

XX	RESULT 10
XX	AAV46462
ID	AAV46462 standard; cDNA; 5711 BP.
XX	
AC	AAV46462;
XX	
DT	18-NOV-1998 (first entry)
XX	
DE	Human BRCA1 omi2 polymorphism #5 cDNA.
XX	
KW	BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
KM	polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW	chromosome 17q; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	120..5711
FT	/tag= a
FT	/product= "BRCA1 omi2 protein"
FT	3667
FT	/tag= b
FT	/note= "This polymorphic variation can be an A or G
FT	nucleotide"
XX	
PN	US5750400-A.
XX	
PD	12-MAY-1998.
XX	
PF	12-FEB-1997; 97US-0798691.
XX	
PR	12-FEB-1996; 96US-0598591.
PR	12-FEB-1997; 97US-0798691.
XX	
PA	(ONCO-) ONCORMED INC.
PI	Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,
PI	Scheitler DB, Zeng B;
XX	
DR	WPI; 1998-236774/26.
XX	

Db 1981 ATGCGCTGAACCTAGTAGTACAGTAAGTCTAAGCCCACTATATGTAATTCGAA 2040
QY 2041 TTGATAGTTGTTTACAGAGTGAAGATTAAGAAAAAGTAAACCAATCCAGTCA 2100
Db 2041 TTGATAGTTGTTTACAGAGTGAAGATTAAGAAAAAGTAAACCAATCCAGTCA 2100
QY 2101 GGCACAGCAGAAACCTACAACTCATGGAAGGTAAAGAACTGCACTGGAGCCCAAGT 2160
Db 2101 GGCACAGCAGAAACCTACAACTCATGGAAGGTAAAGAACTGCACTGGAGCCCAAGT 2160
QY 2161 GTAAACAGCCAAATGAAGACAGACAGTAAGAACATGACAGTACTTTCCAGAGCTGA 2220
Db 2161 GTAAACAGCCAAATGAAGACAGACAGTAAGAACATGACAGTACTTTCCAGAGCTGA 2220
QY 2221 AGTTAAACAAATGCACTGGTCTTTTAACTTAAAGTTCCTAATACAGTGAAT 2280
Db 2221 AGTTAAACAAATGCACTGGTCTTTTAACTTAAAGTTCCTAATACAGTGAAT 2280
QY 2281 TTGTCATCTGCTAGCTTCCAGAGAAAGAAAGAAAGAAAGTAAAGTAAAGT 2340
Db 2281 TTGTCATCTGCTAGCTTCCAGAGAAAGAAAGAAAGAAAGTAAAGTAAAGT 2340
QY 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAGGTTTGCAGAGT 2400
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAGGTTTGCAGAGT 2400
QY 2401 AAAGATCTGTAAGAGTAGAGTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db 2401 AAAGATCTGTAAGAGTAGAGTATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
QY 2461 AAAGATCTGCTAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2520
Db 2461 AAAGATCTGCTAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2520
QY 2521 GTGTCAGTCACTGTCAGTATTTGAAACCCCAAGGACTAATTCATGTTTCTCAAG 2580
Db 2521 GTGTCAGTCACTGTCAGTATTTGAAACCCCAAGGACTAATTCATGTTTCTCAAG 2580
QY 2581 ATAAATGAAGTGAACAGAAAGGCTTTAAGTATTCATTTGGAGCATGAAGTTAACCAAGT 2640
Db 2581 ATAAATGAAGTGAACAGAAAGGCTTTAAGTATTCATTTGGAGCATGAAGTTAACCAAGT 2640
QY 2641 GGGAAACAAGCATAGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
Db 2641 GGGAAACAAGCATAGAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
QY 2701 TCAAGGTTTCAAGCGCCAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Db 2701 TCAAGGTTTCAAGCGCCAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
QY 2761 AATGTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
Db 2761 AATGTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
QY 2821 TTGAATGTAAGAAAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2880
Db 2821 TTGAATGTAAGAAAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2880
QY 2881 AGACAGTTAATCTGTCAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db 2881 AGACAGTTAATCTGTCAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
QY 2941 ATGTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 ATGTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
QY 3001 ACAGAACTGAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Db 3001 ACAGAACTGAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
QY 3061 CACCACTTTTCCATCAAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
Db 3061 CACCACTTTTCCATCAAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120

QY 3121 AAAAATTGAGAGACATTTCAATGCACTGAAAGAAATGGGAAATGGAACATTTCCA 3180
Db 3121 AAAAATTGAGAGACATTTCAATGCACTGAAAGAAATGGGAAATGGAACATTTCCA 3180
QY 3181 GTACAGTGAAGCAATTTAGCCGTAATTAACATTAGAGAAATGTTTAAAGAACCCAGCT 3240
Db 3181 GTACAGTGAAGCAATTTAGCCGTAATTAACATTAGAGAAATGTTTAAAGAACCCAGCT 3240
QY 3241 CAAGCAATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGCTCAGTATTAATGA 3300
Db 3241 CAAGCAATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGCTCAGTATTAATGA 3300
QY 3301 TAGGTTCCAGTATGAAGAAATTTCAAGCAAGAACTAGTGAAGAAAGAGGCCCCAAATTTGA 3360
Db 3301 TAGGTTCCAGTATGAAGAAATTTCAAGCAAGAACTAGTGAAGAAAGAGGCCCCAAATTTGA 3360
QY 3361 ATGCTATGCTTATGATTAAGGAGGTTTTCAGACCTGAGGCTTATAACCAAGTCTTCTGGA 3420
Db 3361 ATGCTATGCTTATGATTAAGGAGGTTTTCAGACCTGAGGCTTATAACCAAGTCTTCTGGA 3420
QY 3421 GTAAATTTGAAGATCTGTAATTAAGAAAGCAAGATTAAGAGTAGTTCAGACTGTTA 3480
Db 3421 GTAAATTTGAAGATCTGTAATTAAGAAAGCAAGATTAAGAGTAGTTCAGACTGTTA 3480
QY 3481 ATACAGATTTCTCCATATCTGATTTTCAATTAAGTGAAGAGGCTTATGAGAGT 3540
Db 3481 ATACAGATTTCTCCATATCTGATTTTCAATTAAGTGAAGAGGCTTATGAGAGT 3540
QY 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGTAGTAGTGAATTAAG 3600
Db 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGTAGTAGTGAATTAAG 3600
QY 3601 AAGATCTAGTTTGTCTGAGAAATGACATTAAGAAAGTCTGCTGTTTACGAAAGG 3660
Db 3601 AAGATCTAGTTTGTCTGAGAAATGACATTAAGAAAGTCTGCTGTTTACGAAAGG 3660
QY 3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGGCTTTCACCAATACATTTGGCTCAG 3720
Db 3661 TCCAGAAAGAGAGCTTACAGAGAGTCTAGGCTTTCACCAATACATTTGGCTCAG 3720
QY 3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780
Db 3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTAGAGATG 3780
QY 3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGGTAAAGTAAACATTAATCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAACTTGTATTTGGTAAAGTAAACATTAATCTTCTCAGT 3840
QY 3841 CTAACTAGGATAGCAACGTTGCTAGCAGAGTCTGCTAAGAACACAGAGAGAAATTTAT 3900
Db 3841 CTAACTAGGATAGCAACGTTGCTAGCAGAGTCTGCTAAGAACACAGAGAGAAATTTAT 3900
QY 3901 TATCATTTGAAGATTAAGCTTAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3960
Db 3901 TATCATTTGAAGATTAAGCTTAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3960
QY 3961 AGGAACATCACTTAAGTGAAGAAACAAATGTTCTGCTGCTGCTTCTTCAAGTGA 4020
Db 3961 AGGAACATCACTTAAGTGAAGAAACAAATGTTCTGCTGCTGCTTCTTCAAGTGA 4020
QY 4021 GTGAATTTGAAGACTGACCTGCAATTAAGAAACCCAGAGTCTTCTGATGTTGTTCT 4080
Db 4021 GTGAATTTGAAGACTGACCTGCAATTAAGAAACCCAGAGTCTTCTGATGTTGTTCT 4080
QY 4081 CCAAACTGAAGCATCACTGTAAGCCAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4140
Db 4081 CCAAACTGAAGCATCACTGTAAGCCAGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4140
QY 4141 TTTCAATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATCAAGAGAGCAAGCA 4200
Db 4141 TTTCAATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATCAAGAGAGCAAGCA 4200

CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi2 gene represented in AAIV46449.

XX Sequence 5711 BP, 1955 A; 1098 C; 1274 G; 1383 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCGACACAGCTGTGGGTTTCTCAGATAACGAGCC 60
DB 1 AGCTGCTGAGACTTCTGAGACCCGACACAGCTGTGGGTTTCTCAGATAACGAGCC 60
QY 61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTGGAACGAAAGAA 120
DB 61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTGGAACGAAAGAA 120
QY 121 TGAATTTATCTGCTCTGCGCGTTGAAGAGTACAAATGTCAATATGCTATGCAAGAA 180
DB 121 TGAATTTATCTGCTCTGCGCGTTGAAGAGTACAAATGTCAATATGCTATGCAAGAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTGTATCAGAGAACCTGTCTCCAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTGTATCAGAGAACCTGTCTCCAAAGTGTGACC 240
QY 241 ACATATTTTGGAAATTTTGCATGCTGAAACCTTCTCAACGAGAAAGGCGCTTCAACT 300
DB 241 ACATATTTTGGAAATTTTGCATGCTGAAACCTTCTCAACGAGAAAGGCGCTTCAACT 300
QY 301 GTCCCTTATGTAAGATATATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTAGTC 360
DB 301 GTCCCTTATGTAAGATATATTAACCAAAAGAGCCTACAAAGAAAGTACGAGATTAGTC 360
QY 361 AACTTGTGAAGAGCTATTAAGAAATCAATTTGTCTTTCAGCTTGAACACAGGTTTGAAT 420
DB 361 AACTTGTGAAGAGCTATTAAGAAATCAATTTGTCTTTCAGCTTGAACACAGGTTTGAAT 420
QY 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480
DB 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540
QY 541 AACCAGAAATCTTCTCTTGGAGAAACCAAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
DB 541 AACCAGAAATCTTCTCTTGGAGAAACCAAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
QY 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATTAACAACCTCAAAAGCGTCTGTCAATTG 660
DB 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATTAACAACCTCAAAAGCGTCTGTCAATTG 660
QY 661 AATTGGGATCTGATCTCTCTGAGAGTACCGTTAATTAAGCAACTTATGCACTGTGGAG 720
DB 661 AATTGGGATCTGATCTCTCTGAGAGTACCGTTAATTAAGCAACTTATGCACTGTGGAG 720
QY 721 ATCAAGAAATTTGTAACAAATCAACCCCTCAAGGAAACAGGAGTGAATCAAGTTGATTCG 780
DB 721 ATCAAGAAATTTGTAACAAATCAACCCCTCAAGGAAACAGGAGTGAATCAAGTTGATTCG 780
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGAACAAATCTGAAACATCTCAAC 840
DB 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGAACAAATCTGAAACATCTCAAC 840
QY 841 CCAATTAATATGATTTGAAACCACTGAGAGCGTGAAGGAGGATCCAGAAAGT 900
DB 841 CCAATTAATATGATTTGAAACCACTGAGAGCGTGAAGGAGGATCCAGAAAGT 900
QY 901 ATCAGGGTAGTCTGTTCAAACTTGATGTGAGACCATGTGGCAAAATACTCATGGCA 960

DB 901 ATCAGGGTAGTCTGTTCAAACTTGATGTGAGACCATGTGGCAAAATACTCATGGCA 960
QY 961 GGTCAATTCAGATGAGAACGAGCTTATTAATCACTAAAGACAGATGATAGTAA 1020
DB 961 GGTCAATTCAGATGAGAACGAGCTTATTAATCACTAAAGACAGATGATAGTAA 1020
QY 961 GGTCAATTCAGATGAGAACGAGCTTATTAATCACTAAAGACAGATGATAGTAA 1020
DB 961 GGTCAATTCAGATGAGAACGAGCTTATTAATCACTAAAGACAGATGATAGTAA 1020
QY 1021 AGGCTGAATTCGTATATTAAGAAACAGCGCTGCTTGAAGAGGCAACATTAACAT 1080
DB 1021 AGGCTGAATTCGTATATTAAGAAACAGCGCTGCTTGAAGAGGCAACATTAACAT 1080
QY 1081 GGGCTGGAAGTAAAGAAACATGTATATGATAGCGGACTCCAGACAGAAAGGATG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGTATATGATAGCGGACTCCAGACAGAAAGGATG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATTAACAGAAACCTGCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATTAACAGAAACCTGCATGCT 1200
QY 1201 CAGAGAAATCTAGAGATCTAGAGATGTTCTTGTGATTAACATTAATAGACATTCAGA 1260
DB 1201 CAGAGAAATCTAGAGATCTAGAGATGTTCTTGTGATTAACATTAATAGACATTCAGA 1260
QY 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGAACTGTAGGTTCTGATGACTCATGATG 1320
DB 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGAACTGTAGGTTCTGATGACTCATGATG 1320
QY 1321 GGGAGTCTGAATCAATGCCAAAGTATGATGATTTGAGCGTTCTAAATGAGTATAGT 1380
DB 1321 GGGAGTCTGAATCAATGCCAAAGTATGATGATTTGAGCGTTCTAAATGAGTATAGT 1380
QY 1381 AATATTCGTGTTCTTCAGAGAAATAGACTTACTGAGCAGTATCTCATGAGCTTTAA 1440
DB 1381 AATATTCGTGTTCTTCAGAGAAATAGACTTACTGAGCAGTATCTCATGAGCTTTAA 1440
QY 1441 TATGTAAAGTGAAGAGTTCATCTCAATCAGTGAAGATTAATTTGAAGACAAATAT 1500
DB 1441 TATGTAAAGTGAAGAGTTCATCTCAATCAGTGAAGATTAATTTGAAGACAAATAT 1500
QY 1501 TTGGGAAACCTATCGGAAGAGGCAAGCCCTCCCACTTAAGCATTAATGAAATATC 1560
DB 1501 TTGGGAAACCTATCGGAAGAGGCAAGCCCTCCCACTTAAGCATTAATGAAATATC 1560
QY 1561 TAAATTAAGAGACTTGTCTAGAGCAGATTAATTAAGAGCGTCCCTCAACAATA 1620
DB 1561 TAAATTAAGAGACTTGTCTAGAGCAGATTAATTAAGAGCGTCCCTCAACAATA 1620
QY 1621 AATTAAAGCGTAAAGAGAGCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680
DB 1621 AATTAAAGCGTAAAGAGAGCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGGAGTCAAAAGACTCTCGAATTAATTAAGGAACTTAACCAAGGAGC 1740
DB 1681 CAGATTTGGGAGTCAAAAGACTCTCGAATTAATTAAGGAACTTAACCAAGGAGC 1740
QY 1741 AGAATGTGCAAGTATGAATTTACTAATAGTGTCTATGAGAAATTAAGAAAGGATG 1800
DB 1741 AGAATGTGCAAGTATGAATTTACTAATAGTGTCTATGAGAAATTAAGAAAGGATG 1800
QY 1801 CTATTCAGATGAGAAATCTTAACCAATTAAGATCACTCGAAAGAAATCTGCTTTCA 1860
DB 1801 CTATTCAGATGAGAAATCTTAACCAATTAAGATCACTCGAAAGAAATCTGCTTTCA 1860
QY 1861 AAAGGAAAGCTGAACCTTAAGAGAGGAGTAAAGCAATTAAGCAATTAAGCAATTAAG 1920
DB 1861 AAAGGAAAGCTGAACCTTAAGAGAGGAGTAAAGCAATTAAGCAATTAAGCAATTAAG 1920
QY 1921 ACAATTCAGAAAGCCTTAAGAAAGATAGCTGAGAGAGAGTCTTCTACAGGACATATTC 1980
DB 1921 ACAATTCAGAAAGCCTTAAGAAAGATAGCTGAGAGAGAGTCTTCTACAGGACATATTC 1980
QY 1981 ATGCGCTTGAATCTAGTATGATGAATCTTAAGCCCACTTAATGTACTGAATTCGAA 2040

ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCTGACACCCCGACACAGCGTGTGGGGTTTCTCAGATTAACCTGGCC 60
DB 1 AGCTCGCTGAGACTTCTCTGACACCCCGACACAGCGTGTGGGGTTTCTCAGATTAACCTGGCC 60
QY 61 CTTGGCGTCAAGAGGCGCTTCAACCTCTGCTGGGTAAATTCATTGGAAACAGAAAGAA 120
DB 61 CTTGGCGTCAAGAGGCGCTTCAACCTCTGCTGGGTAAATTCATTGGAAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTCGCGTTGAAGAGTAACAAATGTCATTATGCTATGACAGAAA 180
DB 121 TGGATTATCTGCTCTCGCGTTGAAGAGTAACAAATGTCATTATGCTATGACAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC 240
QY 241 ACATATTTGCAAAATTTTGATGCTGAACTTCTCAACAGAAAGAAAGGCGCTTCAACAT 300
DB 241 ACATATTTGCAAAATTTTGATGCTGAACTTCTCAACAGAAAGAAAGGCGCTTCAACAT 300
QY 301 GTCCCTTATGTAAGATGATATTAACCAAAAGAGCCCTACAAGAAAGTACAGATTTAGTC 360
DB 301 GTCCCTTATGTAAGATGATATTAACCAAAAGAGCCCTACAAGAAAGTACAGATTTAGTC 360
QY 361 AACTTGTGAAGCTATTTGAANAATCATTTGCTTTTCACTTGAACACAGTTTGAAGT 420
DB 361 AACTTGTGAAGCTATTTGAANAATCATTTGCTTTTCACTTGAACACAGTTTGAAGT 420
QY 421 ATGCAAAACAGCTAATTTTGGCAAAAAGAAATACTCTGTAACATCTAAAGATG 480
DB 421 ATGCAAAACAGCTAATTTTGGCAAAAAGAAATACTCTGTAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCAAGATGAGGCTACAGAAACCGTGCCAAAGACTTCTACAGATG 540
DB 481 AAGTTTCTATCATCAAGATGAGGCTACAGAAACCGTGCCAAAGACTTCTACAGATG 540
QY 541 AACCCGAAAATCCTTCTCTGACAGAAACAGTCTCAGTGTCAACTCTCTAACCTTGA 600
DB 541 AACCCGAAAATCCTTCTCTGACAGAAACAGTCTCAGTGTCAACTCTCTAACCTTGA 600
QY 601 CTGTGGAATCTGAGAGCAAAAGCAGGATACAACTCAAAAGAGCTGTCTTAATG 660
DB 601 CTGTGGAATCTGAGAGCAAAAGCAGGATACAACTCAAAAGAGCTGTCTTAATG 660
QY 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTAATGCAAGTGGAG 720
DB 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTAATGCAAGTGGAG 720
QY 721 ATCAAGATTTTACAAATACCCCTCAAGAAACAGGAGTGAATCAAGTTGGATTCTG 780
DB 721 ATCAAGATTTTACAAATACCCCTCAAGAAACAGGAGTGAATCAAGTTGGATTCTG 780
QY 781 CAAAAAAGGCTGTGTAATTTTCTGAGCGGATGAACAAATCTGAACATCATCAAC 840
DB 781 CAAAAAAGGCTGTGTAATTTTCTGAGCGGATGAACAAATCTGAACATCATCAAC 840
QY 841 CAGATTAATATGATTTGAACACCACTGAGAAAGGCTGAGAGGCAATCCAGAAAAT 900
DB 841 CAGATTAATATGATTTGAACACCACTGAGAAAGGCTGAGAGGCAATCCAGAAAAT 900
QY 901 ATGAGGATGTTGTTTCAAATCTGATGTGAGCAATGTGACAAATATCTCATGCCA 960
DB 901 ATGAGGATGTTGTTTCAAATCTGATGTGAGCAATGTGACAAATATCTCATGCCA 960

DB 901 ATCAGGATGTTCTGTTCCAACTTGCAATGTGAGCCATGATGGCACAAAATACTCATGCCA 960
QY 961 GGTCAATTACAGATGAGAACAGAGTTTATCTCACTAAAGACAGAAATGATGAAA 1020
DB 961 GGTCAATTACAGATGAGAACAGAGTTTATCTCACTAAAGACAGAAATGATGAAA 1020
QY 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGGCTTTAGCAAGAGCCAAATACAGAT 1080
DB 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGGCTTTAGCAAGAGCCAAATACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGAACATGATATGATAGCGGACTCCACAGACAGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGAACATGATATGATAGCGGACTCCACAGACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATCTGATCCCTGTGTGAGAAAGAAATGAAATGAACGAAACCTGCCATGCT 1200
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAAAGAAATGAAATGAACGAAACCTGCCATGCT 1200
QY 1201 CAGAGATCTAGAGATCTGAAAGATGTTCTTGGATTAACATTAATAGCAGATTGACA 1260
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QY 1261 AAGTTAATGAGTGTCTTCCAGAGATGAACTGTTAGTTCTGATGCTACATGATG 1320
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QY 1321 GGGAGCTGAATCAAAATGCAAGTAAAGTATGTAAGTGAACGTTCTAAATGAGTATG 1380
DB 1321 GGGAGCTGAATCAAAATGCAAGTAAAGTATGTAAGTGAACGTTCTAAATGAGTATG 1380
QY 1381 AATATTTCTGTTCTTCAAGAAATAAGATTTACTGCGCAGTATCTCTAGAGCTTTAA 1440
DB 1381 AATATTTCTGTTCTTCAAGAAATAAGATTTACTGCGCAGTATCTCTAGAGCTTTAA 1440
QY 1441 TATGTAAAAGTAAAGATTTCACTCAATCACTAGAGATATATTTGAAGCAAAATAT 1500
DB 1441 TATGTAAAAGTAAAGATTTCACTCAATCACTAGAGATATATTTGAAGCAAAATAT 1500
QY 1501 TTGGGAAAACTATGGGAAAGGCAAGCTCCCACTTAAGCCATGTAACCTGAAAATC 1560
DB 1501 TTGGGAAAACTATGGGAAAGGCAAGCTCCCACTTAAGCCATGTAACCTGAAAATC 1560
QY 1561 TAATTATAGGACATTTGTTACTGAGCAACAGATATTAACAAGAGCTCCCTCACAATA 1620
DB 1561 TAATTATAGGACATTTGTTACTGAGCAACAGATATTAACAAGAGCTCCCTCACAATA 1620
QY 1621 AATTAAAGGTAAGAGACCTATCATAGGCTTCTCATCTGAGGATTTTATCAAGAAAG 1680
DB 1621 AATTAAAGGTAAGAGACCTATCATAGGCTTCTCATCTGAGGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGAGTTCAAAAAGCTCCTGAAATGATTAATCAGGGAACCTAACAGAGAGC 1740
DB 1681 CAGATTTGGAGTTCAAAAAGCTCCTGAAATGATTAATCAGGGAACCTAACAGAGAGC 1740
QY 1741 AGAATGCTCAAGTGAATAATTAATATAGTGTCAATGAGAAATTAACAAGAGTGAAT 1800
DB 1741 AGAATGCTCAAGTGAATAATTAATATAGTGTCAATGAGAAATTAACAAGAGTGAAT 1800
QY 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAATCTGCTTTCA 1860
DB 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAATCTGCTTTCA 1860
QY 1861 AAAAGAAAGCTGAACCTTAAGAGCAGATTAATGAGCAATGGAATCTGAATTAATGCC 1920
DB 1861 AAAAGAAAGCTGAACCTTAAGAGCAGATTAATGAGCAATGGAATCTGAATTAATGCC 1920
QY 1921 ACAATTTCAAAAAGCACTTAAGAGGAGGAGAGTCTTCTACAGAGCATATTC 1980
DB 1921 ACAATTTCAAAAAGCACTTAAGAGGAGGAGAGTCTTCTACAGAGCATATTC 1980
QY 1981 ATGCGCTTGAATGATGCTAGTGAATAATCTAAGCCCACTTAATTTGACTGATTTGCAA 2040
DB 1981 ATGCGCTTGAATGATGCTAGTGAATAATCTAAGCCCACTTAATTTGACTGATTTGCAA 2040

OY	2041	TTGATATGTTGTTCTGACGTAGAGAGATTAAGAAAAAAGTACACCAATTECCAGTCA	2100
Dp	2041	TTGATATGTTGTTCTGACGTAGAGAGATTAAGAAAAAAGTACACCAATTECCAGTCA	2100
OY	2101	GGCAGACAGAAAACTTACAACATCATGAAAGGTAAAGAACTGCAACTGAGCCAGAAAGA	2160
Dp	2101	GGCAGACAGAAAACTTACAACATCATGAAAGGTAAAGAACTGCAACTGAGCCAGAAAGA	2160
OY	2161	GTAACAAAGCCAAATGATAACAGACAGTAAAGACATGACGTGATCTTTCCAGAGCTGA	2220
Dp	2161	GTAACAAAGCCAAATGATAACAGACAGTAAAGACATGACGTGATCTTTCCAGAGCTGA	2220
OY	2221	AGTTAAACAAATGACCTGCGTCTTTTACTAAGTGTTCAAATPACAGGTAACTTTAAAGAT	2280
Dp	2221	AGTTAAACAAATGACCTGCGTCTTTTACTAAGTGTTCAAATPACAGGTAACTTTAAAGAT	2280
OY	2281	TTGTCAATCTAGCCCTTCCAGAGAGAAAGAAAGAGAAAACTAGAAAACGTTAAAGTGT	2340
Dp	2281	TTGTCAATCTAGCCCTTCCAGAGAGAAAGAAAGAGAAAACTAGAAAACGTTAAAGTGT	2340
OY	2341	CTAATATATGCTGGAAGACCCCAAAGTCTCATGTTTAAGTGGAGAAAGGTTTTGCCAACTG	2400
Dp	2341	CTAATATATGCTGGAAGACCCCAAAGTCTCATGTTTAAGTGGAGAAAGGTTTTGCCAACTG	2400
OY	2401	AAAGATCTGTAGAGGTAGAGTAAATTTCACTGGTACCTGGATACGATTAATGGAACCTGACG	2460
Dp	2401	AAAGATCTGTAGAGGTAGAGTAAATTTCACTGGTACCTGGATACGATTAATGGAACCTGACG	2460
OY	2461	AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAGGCAAAAAACAGAACCAATTAAT	2520
Dp	2461	AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAGGCAAAAAACAGAACCAATTAAT	2520
OY	2521	GTGAGAGTCAGGTGACACATTTGAAAAACCCAGAGGACTAATTCATGTTGTTCCAAAG	2580
Dp	2521	GTGAGAGTCAGGTGACACATTTGAAAAACCCAGAGGACTAATTCATGTTGTTCCAAAG	2580
OY	2581	ATATATAGAAATGACACAGAGGCTTAAAGTATCCATTGGGACATGAATTAAACACAGTC	2640
Dp	2581	ATATATAGAAATGACACAGAGGCTTAAAGTATCCATTGGGACATGAATTAAACACAGTC	2640
OY	2641	GGGAAACAGACATAGAAAAATGGAAGAAATGGAATTCGATAGTTTGGACAATATCAT	2700
Dp	2641	GGGAAACAGACATAGAAAAATGGAAGAAATGGAATTCGATAGTTTGGACAATATCAT	2700
OY	2701	TCAAGGTTTCAAAGGCGCAGTATTTGCTGTTTTCAAATCCAGGAAATGCAAGAAAGG	2760
Dp	2701	TCAAGGTTTCAAAGGCGCAGTATTTGCTGTTTTCAAATCCAGGAAATGCAAGAAAGG	2760
OY	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGTCTTTAAAGAAAACAAAGTCCAAAGTCACTT	2820
Dp	2761	AATGTGCAACATTTCTCTGCCCACTCTGGGTCTTTAAAGAAAACAAAGTCCAAAGTCACTT	2820
OY	2821	TTGAATGTGAAACAAAAGGAGAGAAATCAAGGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Dp	2821	TTGAATGTGAAACAAAAGGAGAGAAATCAAGGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
OY	2881	AGACAGTTAATATCACTGAGGCTTCCGTGGTGTGGTCAGAAAGATAGCCAGTGTATA	2940
Dp	2881	AGACAGTTAATATCACTGAGGCTTCCGTGGTGTGGTCAGAAAGATAGCCAGTGTATA	2940
OY	2941	ATGCCAAATGTATATCAAAAGAGGCTTAGGTTTTGTCTATCATCTTCAGTTCCAGAGCA	3000
Dp	2941	ATGCCAAATGTATATCAAAAGAGGCTTAGGTTTTGTCTATCATCTTCAGTTCCAGAGCA	3000
OY	3001	ACGAATCTGAGACTATTTACTCCAATTAACAATGACATTTTACAAACCATAATGTATATC	3060
Dp	3001	ACGAATCTGAGACTATTTACTCCAATTAACAATGACATTTTACAAACCATAATGTATATC	3060
OY	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTATAGAAAAATCTGCTAGAGG	3120
Dp	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTATAGAAAAATCTGCTAGAGG	3120

OY	3121	AAAATTGTAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTC	3180
Db	3121	AAAATTGTAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAACATTC	3180
OY	3181	GTACAGTAGACAATTTAGCCGTATAATCAATTAGAGAAATGTTTTTAAAGAGCAGCT	3240
Db	3181	GTACAGTAGACAATTTAGCCGTATAATCAATTAGAGAAATGTTTTTAAAGAGCAGCT	3240
OY	3241	CAAGCAATATTATGAGTAGAGTTCAGTACTTAATGAAATGGGGTCCAGTATTAATGAA	3300
Db	3241	CAAGCAATATTATGAGTAGAGTTCAGTACTTAATGAAATGGGGTCCAGTATTAATGAA	3300
OY	3301	TAGGTTCCAGTAGAATAAACAATCAAGAGAACTTAGAGAAACAGAGGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTAGAATAAACAATCAAGAGAACTTAGAGAAACAGAGGGCCAAATTTGA	3360
OY	3361	ATGCTATGCTTAAGATTAGGGGTTTTGCAACCTGAGTCTATATAACAAAGTCTTCTGGA	3420
Db	3361	ATGCTATGCTTAAGATTAGGGGTTTTGCAACCTGAGTCTATATAACAAAGTCTTCTGGA	3420
OY	3421	GTAAATTGAAACATCTGAAATTAATAAAGCAAGAAATGAAAGAAATGACTGAGCTGTA	3480
Db	3421	GTAAATTGAAACATCTGAAATTAATAAAGCAAGAAATGAAAGAAATGACTGAGCTGTA	3480
OY	3481	ATACAGATTTTCTTCCATATCTGATTTTGAATTAATCTTAGAACACCTATGAGGAATGTC	3540
Db	3481	ATACAGATTTTCTTCCATATCTGATTTTGAATTAATCTTAGAACACCTATGAGGAATGTC	3540
OY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTGATGATGATGTAATAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTGATGATGATGTAATAAGG	3600
OY	3601	AAGATACTAGTTTTGCTGAAAAATGACATTAAGAAAGTTGCTGTTTTTACAAAACCG	3660
Db	3601	AAGATACTAGTTTTGCTGAAAAATGACATTAAGAAAGTTGCTGTTTTTACAAAACCG	3660
OY	3661	TCCAGAGAGGAGACTTGACGAGAGTCTTACACCTTTCACCCATACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGGAGACTTGACGAGAGTCTTACACCTTTCACCCATACATTTGGCTCAGG	3720
OY	3721	GTTACCGAAGAGGGGCCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTAGATG	3780
OY	3781	AAGAGCTTCCCTGCTTCCACACCTTGTATTTTGGTAAAGTAAACATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACACCTTGTATTTTGGTAAAGTAAACATATACCTTCTCAGT	3840
OY	3841	CTACTAGGCAATGACACCGTGTCTACCCGAGTGTCTGTCTTAAGAACACAGAGGAAATTTAT	3900
Db	3841	CTACTAGGCAATGACACCGTGTCTACCCGAGTGTCTGTCTTAAGAACACAGAGGAAATTTAT	3900
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Db	3901	TATCATTAAGAAATAGCTTAATATAGTACGTCACTAACCAGTAACTTATGGCAAGGATCTC	3960
OY	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGTAGCTGTGTTTTCTTCAAGTGA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGTAGCTGTGTTTTCTTCAAGTGA	4020
OY	4021	GTGAATTGGAAGACTTGACTCAATATCAAAACCCAGAGATCTTGTCTTGATTTGGTCTT	4080
Db	4021	GTGAATTGGAAGACTTGACTCAATATCAAAACCCAGAGATCTTGTCTTGATTTGGTCTT	4080
OY	4081	CCAAACAAATAGGCAATCAGTCTGAAGCCAGGGAGTTGCTGTAGTAGCAAGAAATTTGG	4140
Db	4081	CCAAACAAATAGGCAATCAGTCTGAAGCCAGGGAGTTGCTGTAGTAGCAAGAAATTTGG	4140
OY	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAGAGCAAAACA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAGAGCAAAACA	4200
OY	4201	TGGAATTCAAACTTAGTGGAAGACAGCATCTTGGGTGTGAGAGTGAAGAACAGCTCTTGAAG	4260

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5701 GCCACTACTGA 5711
5701 GCCACTACTGA 5711
5701 GCCACTACTGA 5711

RESULT 3
US-08-825-487A-1
; Sequence 1, Application US/08825487A
; Patent No. 6048689
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: White, Margie B.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue., N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,487A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/060002
; FILING DATE: 26-Mar-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 05371, 0012, 999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 STRAIN: BRCA1
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 17
 MAP POSITION: 17q21
 US-08-825-487A-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTGAGACCCCGACACGAGCTGGGGTTCTCAGATTAATCGGGCC 60
 DB 1 AGCTCGCTGAGACTTCTGAGACCCCGACACGAGCTGGGGTTCTCAGATTAATCGGGCC 60
 QY 61 CCTCGCTCAGAGAGGCTTCACTCTGCTGCGTAAAGTTCAATTGAAACAGAAAGAAA 120
 DB 61 CCTCGCTCAGAGAGGCTTCACTCTGCTGCGTAAAGTTCAATTGAAACAGAAAGAAA 120
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 DB 661 AATTGGGATCTGATCTTCTGAGAAATCCGTTAATAGGCACTTAATTCAGGTGGAG 720
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 DB 721 ATCAAGAAATGTTTACAAATCACTTCAAGAAACAGGATGAATCACTTTGATTCG 780
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 DB 781 CAAAAAGAGCTGCTTGTGAATTTTCTGAGACGATGTAACTAATCTGAACATCATCAAC 840
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 DB 961 GCTCATTAACAGATGAGAAACAGAGTTTATTACTCACTAAAGACAGAAATGATAGAAA 1020
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 DB 1021 AGGCTGAATTTCTGTAATTAAGCAACAGCCTGCTTACGAAAGAGGCAATTAACGAT 1080
 QY 1081 GGGCTGAAGTAAGGAAACATGTAATGATAGGCGGACTCCAGCAGAGAAAAAGGTAG 1140
 DB 1081 GGGCTGAAGTAAGGAAACATGTAATGATAGGCGGACTCCAGCAGAGAAAAAGGTAG 1140
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 DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT 1200
 QY 1201 CAGAGAAATCTGAGATATCTGAAGTGTCTTGGATTAACCTTAATTAAGCAGATTGAGA 1260
 DB 1201 CAGAGAAATCTGAGATATCTGAAGTGTCTTGGATTAACCTTAATTAAGCAGATTGAGA 1260
 QY 1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTTAGTTCTGATGACTCATGATAGT 1320
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 QY 1741 AGAATGTCAGAGTGAATTAATTAATGATGCTGATGAGATTAATCAAAAGAGTAT 1800
 DB 1741 AGAATGTCAGAGTGAATTAATTAATGATGCTGATGAGATTAATCAAAAGAGTAT 1800
 QY 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATTAAGATCACTGAAAAAGAAATCTGCTTCA 1860
 DB 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATTAAGATCACTGAAAAAGAAATCTGCTTCA 1860
 QY 1861 AAACGAAAGCTGAACCTTAAGCAGCAGATTAACCAATTAAGATCACTGAAAAAGAAATCTGCTTCA 1920
 DB 1861 AAACGAAAGCTGAACCTTAAGCAGCAGATTAACCAATTAAGATCACTGAAAAAGAAATCTGCTTCA 1920
 QY 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGAGCTTCTTACAGGCAATTC 1980
 DB 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAGAGCTTCTTACAGGCAATTC 1980
 QY 1981 ATGCGCTTGAACCTAGTACTGATGAAATCTTAAGCCCACTTAATTTGATGAAATTCGAAA 2040

Db	1981	ATGCGTTGAACCTAGTACGTAGAAATCTAAGCCACCTTAATGTGACTGAATTGGCAA	2040
Qy	2041	TTGATAGTGTCTCTAGCAAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCGAGTCA	2100
Db	2041	TTGATAGTGTCTCTAGCAAGTGAAGATTAAGAAAAAAAGTACAAACCAATGCGAGTCA	2100
Qy	2101	GGCACAAGCAGAAACCTACACTCATGGAAGGTAAAGAACTTGCAACTGAGCCAGAAAGA	2160
Db	2101	GGCACAAGCAGAAACCTACACTCATGGAAGGTAAAGAACTTGCAACTGAGCCAGAAAGA	2160
Qy	2161	GTACCAAGCCAATGAATGAACGAATTAAGACATGACAGTATCTTTCCAGAGCTGA	2220
Db	2161	GTACCAAGCCAATGAATGAACGAATTAAGACATGACAGTATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAATGACACCTGCTGTTCTTTACTAAGTGTTCAAATACAGTAACTTAAAGAT	2280
Db	2221	AGTTAAACAATGACACCTGCTGTTCTTTACTAAGTGTTCAAATACAGTAACTTAAAGAT	2280
Qy	2281	TTGTCAATCTAGCCTTCCAGAGAAAAAGAGAGAACTAGAAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTAGCCTTCCAGAGAAAAAGAGAGAACTAGAAACAGTTAAAGTGT	2340
Qy	2341	CTAATTAATGCTGAAGACCCCAAAAGTCTCATGTGTAAGTGAAGAGGTTTTGCAACTG	2400
Db	2341	CTAATTAATGCTGAAGACCCCAAAAGTCTCATGTGTAAGTGAAGAGGTTTTGCAACTG	2400
Qy	2401	AAAGATCTGTAGAGATGAGACATATTTCACTGATCCTGGATCTGATTAATGCACTCAG	2460
Db	2401	AAAGATCTGTAGAGATGAGACATATTTCACTGATCCTGGATCTGATTAATGCACTCAG	2460
Qy	2461	AAAGATCTCGTTACTGGAAGTTAGCACTTAGAGGAGCAGAAAAAGCAACCAATTAAT	2520
Db	2461	AAAGATCTCGTTACTGGAAGTTAGCACTTAGAGGAGCAGAAAAAGCAACCAATTAAT	2520
Qy	2521	GTGTGATGACAGTGTGACAGATTTGAAAAACCCCAAGGACATAATTCATGTGTTCCAAAG	2580
Db	2521	GTGTGATGACAGTGTGACAGATTTGAAAAACCCCAAGGACATAATTCATGTGTTCCAAAG	2580
Qy	2581	ATTAATAGAAATGACACAGAAAGGCTTTAGTATTCATTTGGGACATGAATTAACACAGTC	2640
Db	2581	ATTAATAGAAATGACACAGAAAGGCTTTAGTATTCATTTGGGACATGAATTAACACAGTC	2640
Qy	2641	GGGAAACAAGCATAGAAATGGAAGAATGGAATGATGCTCAGTATTTGCAGAAATCAT	2700
Db	2641	GGGAAACAAGCATAGAAATGGAAGAATGGAATGATGCTCAGTATTTGCAGAAATCAT	2700
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Db	2701	TCAAGGTTTCAAAAGCGCCAGTCAATTTGCTGTGTTTCAAAATCCAGAAATCCAGAAAGG	2760
Qy	2761	AATGAGCAACATTTCTGTGCGCACTGTGGTCTTTAAGAAACCAAGTCCAAATCTCT	2820
Db	2761	AATGAGCAACATTTCTGTGCGCACTGTGGTCTTTAAGAAACCAAGTCCAAATCTCT	2820
Qy	2821	TTGAATGTGAACAAAGAGAGAAATCAAGGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGAGAGAAATCAAGGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGCAAGGCTTCTGTGTGTTGTCAAGAAATTAAGCCAGTTGATA	2940
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Qy	2941	ATGCAAAATGATATCAAAAGAGGCTCTAGGTTTGTCTATCAATCTCAGTTCAAGAGCA	3000
Db	2941	ATGCAAAATGATATCAAAAGAGGCTCTAGGTTTGTCTATCAATCTCAGTTCAAGAGCA	3000
Qy	3001	ACGAATCTGACTCATCTACTCCAAATAAATGAGCTTTTACAAACCCATATGATATAC	3060
Db	3001	ACGAATCTGACTCATCTACTCCAAATAAATGAGCTTTTACAAACCCATATGATATAC	3060
Qy	3061	CACCACTTTTCCATCAAGTCAATTTGTTAAAATAATGTAAGAAAAATCTGCTAAGG	3120

Db	3061	CACCACTTTTCCCATCAAGTCATTGTGTTAAACTAAATGTAAAGAAAAATCTGTAAGG	3120
QY	3121	AAAATTTTGAGAACATTCAATGTCACCTGAAGAAATGGAAATGAGAACATTCCA	3180
Db	3121	AAAATTTTGAGGAACATTCAATGTCACCTGAAGAAATGGAAATGAGAACATTCCA	3180
QY	3181	GTACAGTGAACAATTAGCCGTAAATACATTAGAAAAATGTTTTAAAGAGCCACT	3240
Db	3181	GTACAGTGAACAATTAGCCGTAAATACATTAGAAAAATGTTTTAAAGAGCCACT	3240
QY	3241	CAGCAATATTAATGAAGTAGGTCCTACTACTAATGAAGTGGGGCCAGTATTAATGAA	3300
Db	3241	CAGCAATATTAATGAAGTAGGTCCTACTACTAATGAAGTGGGGCCAGTATTAATGAA	3300
QY	3301	TAGGTTCCAGTATGATGAAAAACATTCAAGCAGAACTAGTAGAAACAGAGGCCAAATTGA	3360
Db	3301	TAGGTTCCAGTATGATGAAAAACATTCAAGCAGAACTAGTAGAAACAGAGGCCAAATTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATTAACAAAGTCTTCTGGAA	3420
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5701 GCGACTACTGA 5711

RESULT 4
US-09-074-476-1
Sequence 1, Application US/09074476
Patent No. 6130322
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antoinette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Brenda S.
APPLICANT: Olson, Sheri J.
APPLICANT: Thunder, Denise
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5711 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 STRAIN: BRCA1 (om11)
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 17
 MAP POSITION: 17q21
 US-09-074-476-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4921 AAGTCCCAATTGAAGTTGAGATCTGCGCCAGAGGCTCAGTGTCTGCTCAATCAATG 4980
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DB 5701 GCCACTACTGA 5711

RESULT 5
US-08-798-691-5
Sequence 5, Application US/08798691
Patent No. 5750400
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Brenda S.
APPLICANT: Olson, Sheri J.
APPLICANT: Schelter, Denise B.
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
NUMBER OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONCOMED
STREET: 200 Perry Parkway
CITY: Galthersberg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos

REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-5

Query Match 100.0%; Score: 5709.4; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 721 ATCAAGAAATGTATCAAAATCAACCCCTCAAGAAACAGGATGAATCAGTTTGGATTCTG 780
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DB 5041 CTTCAACGAAAGGCTCAACAAAGATGTCATGATGATGCTGCTGAGAGGAGGAGG 5100
QY 5101 AATTATCTGCTGTATCAAGTTTGCAGAGAAACACACATCACTTAATCTAATTA 5160

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DB 5521 GCACAGGTGTCCACCAATTTGTGTGTGACCAAGTCTGTGAGAGGAGATGAGT 5580
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DB 5581 TCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTAAGAGGAGTGTGAGTGA 5640
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DB 5641 GTTGAACACTTACCAAGTCCAGAGAGCTGACACCTTACCTGATACCCAGATCCCA 5700
QY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711

RESULT 6
US-08-825-487A-5
Sequence 5, Application US/08825487A
Patent No. 6048689
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: White, Marga B.
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC.
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSER: Howrey & Simon
STREET: 1299 Pennsylvania Avenue., N.W.
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,487A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/060002
FILING DATE: 26-Mar-1998
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Albert P. Halluin
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 05371.0012.999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-463-8100
 TELEFAX: 650-463-8400
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5711 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 STRAIN: BRC41
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 17
 MAP POSITION: 17q21
 US-08-825-487A-5

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTCTCTGAGACCCCGACACGAGCTGTGGGTTTCTCAGATACTGGGCC 60
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 DB 481 AAGTTTCTATCATCAAAAGATGTGGCTACAGAAACCGTGCAGAAAGATCTTACAGAGTG 540
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 DB 541 AACCCGAAATCTTCTCTGAGAGAAACAGCTCAAGTGTCAACCTCTAAACCTTGGAA 600
 QY 601 CTGTGGAACCTCTGAGAGCAAAAGCAGGATACAACTCAAAAGAGCTGTCTTACATTTG 660
 DB 601 CTGTGGAACCTCTGAGAGCAAAAGCAGGATACAACTCAAAAGAGCTGTCTTACATTTG 660
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 DB 661 AATTGGATCTGATTTCTTGAAGATACCGTTATTAAGCACTTATTTGAGAGTGTGGAG 720

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 DB 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACGAGGATGAATCAAGTTGGATTCTG 780
 QY 781 CAAAAAGAGCTGTTGTGAATTTTCTGAGACGATGTAACAATACTGAACATCATCAAC 840
 DB 781 CAAAAAGAGCTGTTGTGAATTTTCTGAGACGATGTAACAATACTGAACATCATCAAC 840
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 DB 841 CCAATTAATATGATTTTGAACACCACTGAGAGAGCTGACGTAGAGGCTCCAGAAAGT 900
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 DB 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGAGAGCATGTGGCAAAATPACTCAGGCA 960
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 DB 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGAATGTAGAAA 1020
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 DB 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCCAAGACAGAAAAAGGTAG 1140
 QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGAATGAAGCAAACTGCCATGCT 1200
 DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGAATGAAGCAAACTGCCATGCT 1200
 QY 1201 CAGAGAAATCTTGAAGTACTGAAGATGTTCTTGGATTAACCTAATAGCAGATTCAGA 1260
 DB 1201 CAGAGAAATCTTGAAGTACTGAAGATGTTCTTGGATTAACCTAATAGCAGATTCAGA 1260
 QY 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAAGCTGTGAGTCTGATGACCTACATGAGT 1320
 DB 1261 AAGTTAATGAGTGTGTTTCCAGAGTGAAGCTGTGAGTCTGATGACCTACATGAGT 1320
 QY 1321 GGGAGTCTGAATCAATGCAAGTGAAGTGAATTTGAGCCTTCAATTAAGAGTAGATG 1380
 DB 1321 GGGAGTCTGAATCAATGCAAGTGAAGTGAATTTGAGCCTTCAATTAAGAGTAGATG 1380
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 QY 1441 TATGTAAAGTGAAGAGTGTCTCCAAATCAGTGAAGTAAATTTGAAGCAAAATAT 1500
 DB 1441 TATGTAAAGTGAAGAGTGTCTCCAAATCAGTGAAGTAAATTTGAAGCAAAATAT 1500
 QY 1501 TTGGGAAAACTTATGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAACTGAAAAATC 1560
 DB 1501 TTGGGAAAACTTATGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAACTGAAAAATC 1560
 QY 1561 TAAATTAAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGGCTCCCTCACAAATA 1620
 DB 1561 TAAATTAAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGGCTCCCTCACAAATA 1620
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 DB 1621 AATTAAAGGTAAAGAGAGCTTACATAGAGCTTCACTCTGAGAGATTTTATCAAGAAAG 1680
 QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATTAATCAGGGAACCTAACCGAGAGC 1740
 DB 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATGATTAATCAGGGAACCTAACCGAGAGC 1740
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 DB 1741 AGAATGCTCAAGTATGAATTAATTAATGATGCTATGAGAAATTAACCAAAAGGTGATT 1800

QY 1801 CTATTGAGATGAGAAAAATCCCTAACCCTAGTAATCACTCGAAAAAGAAATCGCTTCA 1860
DB 1801 CTATTGAGATGAGAAAAATCCCTAACCCTAGTAATCACTCGAAAAAGAAATCGCTTCA 1860
QY 1861 AAAGGAAAGCTGAACTTAATAGCAGCAGATATAGCAATATGAAATCGAATTAATATCC 1920
DB 1861 AAAGGAAAGCTGAACTTAATAGCAGCAGATATAGCAATATGAAATCGAATTAATATCC 1920
QY 1921 ACAATTTCAAAAGCAGCTTAAAAAGATAGGCTGAGAGAAAGTCTTACCAGGCAATATTC 1980
DB 1921 ACAATTTCAAAAGCAGCTTAAAAAGATAGGCTGAGAGAAAGTCTTACCAGGCAATATTC 1980
QY 1981 ATGGGCTTGAAGCTAGTACTAGTAAATCTAAGCCCACTAATTTGATCTGAATTTGCAAA 2040
DB 1981 ATGGGCTTGAAGCTAGTACTAGTAAATCTAAGCCCACTAATTTGATCTGAATTTGCAAA 2040
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACAACCAATGCCAGTCA 2100
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACAACCAATGCCAGTCA 2100
QY 2101 GGCACAGAGAAACCTACACCTCATAGAAAGTAAAGAACTTGCAACTGAGAGCCAGAA 2160
DB 2101 GGCACAGAGAAACCTACACCTCATAGAAAGTAAAGAACTTGCAACTGAGAGCCAGAA 2160
QY 2161 GTAACAAAGCCAAATGAACAGACAAATTAAGACATGACAGTATCTTCCAGAGCTGA 2220
DB 2161 GTAACAAAGCCAAATGAACAGACAAATTAAGACATGACAGTATCTTCCAGAGCTGA 2220
QY 2221 AGTTAAACAATGACACCTGGTCTTTTACTAAGTGTCAAAATACCAAGTGAATTAAGAAAT 2280
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QY 2341 CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG 2400
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QY 2401 AAAAGTCTGTAGAGTAGACATTAATTCATCTGGTACTGATTAATGCACTCAGG 2460
DB 2401 AAAAGTCTGTAGAGTAGACATTAATTCATCTGGTACTGATTAATGCACTCAGG 2460
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DB 2641 GGGAAACAGAGCTAGAAATGAGAAAGAAAGTGAATCTGATCTGATTTGTCGAGAAATACAT 2700
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DB 2701 TCAAGGTTTCAAAAGGCCAGTCAATTTGCTCTGTTTCAATCCAGGAAATGCGAAGAGG 2760
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DB 2821 TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGAAATGAGTATATCAAGCCGTATC 2880
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DB 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTTGCTGAGAAAGATTAAGCCAGTTGATA 2940
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DB 3121 AAACTTTGAGGAACATTCATATGTCACCTGAAAGAAATGGGAAATGAGAACATTCOA 3180
QY 3181 GTACAGTGAAGCAATTAAGCCGTAAATTAACATTAAGAAATGTTTTPAAGAGCCAGCT 3240
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QY 3301 TAGGTTCCAGGATGTAACAAATTCAGAGAGAACTGATGTAAGAAACAGAGGCCAAATTTGA 3360
DB 3301 TAGGTTCCAGGATGTAACAAATTCAGAGAGAACTGATGTAAGAAACAGAGGCCAAATTTGA 3360
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QY 3481 ATACAGATTTCTCTCATATCTGATTTGATTAATTAAGTGAACAGCTTAAGGAAATGTC 3540
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QY 3541 ATGCAATCTCAGGTTGTTCTGAGACACCTGATGACCTGTATGATGATGTTAAATTAAG 3600
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QY 3601 AAGATTAATGATTGCTGAAATGACATTAAGAAAGTGTCTGCTGTTTATGCAAAAGCG 3660
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QY 3721 GTTACCGAAGAGGAGGCGCAAGAAATTAAGTCTTCAAGAAAGAACTTAATCTGAGGATG 3780
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QY 3781 AAGAGCTTCCGCTTCCAAACATTTGTTAAGTAAAGTAAATATACCTTCTCAGT 3840
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QY 3841 CTACTAGCATGACACCGTGTGACCGAGTCTGTCTAAGAACACAGAGAGAAATTAAT 3900
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QY 3901 TATCATTTGAAGATATGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3960
DB 3901 TATCATTTGAAGATATGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3960
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QY 4081 CCAACAAATGAGGATCAGTCTGAAAGCCAGGAGTGTGCTGAGTGAACAGAAATTGG 4140
Db 4081 CCAACAAATGAGGATCAGTCTGAAAGCCAGGAGTGTGCTGAGTGAACAGAAATTGG 4140
QY 4141 TTTCATATGATGAAGAAAGAGAAACGGGCTTGAAGAAATAATCAAGAAAGCAAGCA 4200
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QY 4201 TGGATTCAACTAAGTGAAGAGCATCTGGGCTGAGTGAAGCAAGGCTCTGAGG 4260
Db 4201 TGGATTCAACTAAGTGAAGAGCATCTGGGCTGAGTGAAGCAAGGCTCTGAGG 4260
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGATACCATGC 4320
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGATACCATGC 4320
QY 4321 AACATTAAGTGAAGAGCTCAGAGGAAATGGCTGAATAGAGCTGTGTTGAACAGC 4380
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QY 4501 GTGAATACCTTATACAGGAAATCCAGAAAGGCTTCTGCTGCAAGTTGAGTGTCTG 4560
Db 4501 GTGAATACCTTATACAGGAAATCCAGAAAGGCTTCTGCTGCAAGTTGAGTGTCTG 4560
QY 4561 CAGATAGTCTTACAGTAAATAATTAAGAAACAGAGTGAAGAGTATCCCTCTTAAT 4620
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QY 4621 GCCCATCATTAAGTGAAGTGTGATCATGACAGTGTCTCTGAGATCTTCAAGATAGA 4680
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QY 4681 ACTAACCATTCTCAAGAGAGCTCATTAAGTGTGATGAGAGCAACAGCTGGAAG 4740
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Db 4921 AAGTCCCAATGGAAGTGTGCAAGTCTGCGGAGGCTCAGTGTGCTCACTACTG 4980
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QY 5101 AATTATGCTCGTGTACAAAGTTTGCAGAAACACCAATCACTTAATCTAATTA 5160
Db 5101 AATTATGCTCGTGTGTACAAAGTTTGCAGAAACACCAATCACTTAATCTAATTA 5160
QY 5161 CTGAAGAGACTCATGTTGTTATGAAACAGATGCTGAGTGTGTGTGAACGAGAC 5220
Db 5161 CTGAAGAGACTCATGTTGTTATGAAACAGATGCTGAGTGTGTGTGAACGAGAC 5220
QY 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGTATGTTGCTATTTCTGGTGAAC 5280
Db 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGTATGTTGCTATTTCTGGTGAAC 5280
QY 5281 AGCTATTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGATGTGG 5340
Db 5281 AGCTATTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGATGTGG 5340
QY 5341 TCAATGGAAGAAACCAAGGCTCCAAAGCAGAGCAAGAGATCCAGACAGAAAGATCT 5400
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QY 5461 AATGATGTTACAGCTGTGTGCTCTGTGTGTAAGAGCTTTCATGATCACCCTTG 5520
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Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGTGTGACA 5640
QY 5641 GTGTAGCACTTACAGGTCAGAGGCTGAGACCTGATCTGATCCCGAGATCCCGACA 5700
Db 5641 GTGTAGCACTTACAGGTCAGAGGCTGAGACCTGATCTGATCCCGAGATCCCGACA 5700
QY 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 7
US-09-074-476-3
; Sequence 3, Application US/09074476
; Patent No. 6130322
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvarez, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Thumber, Denise
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N. W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL (om12)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-3

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGGAACCCCGCACAGGCTGTGGGTTTCTCAATATACCTGGCC 60
DB 1 AGCTGCTGAGACTTCTGGAACCCCGCACAGGCTGTGGGTTTCTCAATATACCTGGCC 60
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DB 121 TGAATTTATCTGCTCTTGGCGTTGAAGAGTACAAATGTCTAATGCTATGCAAGAAA 180
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DB 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGGAACCTGTCTCCAAAGGTGTGACC 240
QY 241 ACATATTTTGGAAATTTTGCATGCTGAAACCTCTCAACGAGAAAGAGGCTTTCACAGT 300
DB 241 ACATATTTTGGAAATTTTGCATGCTGAAACCTCTCTCAACGAGAAAGAGGCTTTCACAGT 300
QY 301 GTCCCTTATGTAAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
DB 301 GTCCCTTATGTAAGATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360
QY 361 AACTTGTGAAGAGCTATTTGAAATCATTTGTGCTTTTCACTTGCACAGGTTTGGAGT 420
DB 361 AACTTGTGAAGAGCTATTTGAAATCATTTGTGCTTTTCACTTGCACAGGTTTGGAGT 420
QY 421 ATGCAAAAGAGCTATTTTGGCAAAAAGAGAAATTAACCTCTCTGAAACATCTTAAAGATG 480
DB 421 ATGCAAAAGAGCTATTTTGGCAAAAAGAGAAATTAACCTCTCTGAAACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACGGTGCAGAAAGACTTCTTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACGGTGCAGAAAGACTTCTTACAGAGTG 540
QY 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTCAGTGTCCAATCTCTTAACTTTGAA 600
DB 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTCAGTGTCCAATCTCTTAACTTTGAA 600

QY 601 CTGTGAGAACTCTGAGCAAAAGAGCGGATACAACTCAAAAGACGTCTGTACATTTG 660
DB 601 CTGTGAGAACTCTGAGCAAAAGAGCGGATACAACTCAAAAGACGTCTGTACATTTG 660
QY 661 AATTGGATCTGATTTCTTCTGAGATACCGTTAATTAAGCAACTTATTTGACGTGGAG 720
DB 661 AATTGGATCTGATTTCTTCTGAGATACCGTTAATTAAGCAACTTATTTGACGTGGAG 720
QY 721 ATCAAGATTTGTAACAAATCAACCTTCAAGGACCAAGGATGAATATGATTTGATCTG 780
DB 721 ATCAAGATTTGTAACAAATCAACCTTCAAGGACCAAGGATGAATATGATTTGATCTG 780
QY 781 CAAAAAGAGCTCTGTAATTTTCTGAGAGGATGTAACTAAATCTGAACATCATCAAC 840
DB 781 CAAAAAGAGCTCTGTAATTTTCTGAGAGGATGTAACTAAATCTGAACATCATCAAC 840
QY 841 CCAATTAATTAATGATTTGAAACCACTGAGAAAGCGTGACGCTGAGAGGATTCAGAAAAGT 900
DB 841 CCAATTAATTAATGATTTGAAACCACTGAGAAAGCGTGACGCTGAGAGGATTCAGAAAAGT 900
QY 901 ATCAGGATAGTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960
DB 901 ATCAGGATAGTTCTGTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960
QY 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTAATCACTAAGACAGAAATGATAGAA 1020
DB 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTAATCACTAAGACAGAAATGATAGAA 1020
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAAGCCTGCTTACAGAGAGCCCAATTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAAGCCTGCTTACAGAGAGCCCAATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGCCGACCTCCAGACACGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGCCGACCTCCAGACACGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAGAAATCTGCATGCT 1200
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAGAAATCTGCATGCT 1200
QY 1201 CAGAGAAATCTGAGATACGTAAGATGTTCTTGGATTAACCTAATTAAGCAGATTTAGA 1260
DB 1201 CAGAGAAATCTGAGATACGTAAGATGTTCTTGGATTAACCTAATTAAGCAGATTTAGA 1260
QY 1261 AAGTTAAGAGTGTCTTCCAGAGTGAATGTAAGTGTGATGATGATGATGATGATGATG 1320
DB 1261 AAGTTAAGAGTGTCTTCCAGAGTGAATGTAAGTGTGATGATGATGATGATGATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTACGTAATTTGAGAGCTTCTAATAGGTAGATG 1380
DB 1321 GGGAGTCTGAATCAAAATCCAAAGTACGTAATTTGAGAGCTTCTAATAGGTAGATG 1380
QY 1381 AATATTTGCTTCTTCAAGAAATATAGCTTACTGCGCAGTATCTCATGAGCTTTAA 1440
DB 1381 AATATTTGCTTCTTCAAGAAATATAGCTTACTGCGCAGTATCTCATGAGCTTTAA 1440
QY 1441 TATGTAAGTGAAGAGTATCTTCAATCCAAATAGTGAAGATTAATTAAGCAAAATAT 1500
DB 1441 TATGTAAGTGAAGAGTATCTTCAATCCAAATAGTGAAGATTAATTAAGCAAAATAT 1500
QY 1501 TTGGGAAACCTATGCGAAGAGCAAGCCTCCCACTTAAGCATGTAACGTAATC 1560
DB 1501 TTGGGAAACCTATGCGAAGAGCAAGCCTCCCACTTAAGCATGTAACGTAATC 1560
QY 1561 TAAATTAAGAGACTTTGTACTGAGCCACAGATTAATTAAGAGCGTCTCCCAATA 1620
DB 1561 TAAATTAAGAGACTTTGTACTGAGCCACAGATTAATTAAGAGCGTCTCCCAATA 1620
QY 1621 AATTAAAGCTTAAGAGAGCTCATGAGGCTTCAATCTGAGAGATTTTATCAAGAAAG 1680
DB 1621 AATTAAAGCTTAAGAGAGCTCATGAGGCTTCAATCTGAGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATTAATCAAGGAATTAACCAAGAGC 1740

Db 1681 CAAATTGGCAGTTCAAAAGACTCTCGAAATGATTAATCAGGAACTAACCAACGAGC 1740
Qy 1741 AGAATGCTCAAGTAGAATAATTAATAATAGTGTCTAGAAATTAACAAAGAGATT 1800
Db 1741 AGAATGCTCAAGTAGAATAATTAATAATAGTGTCTAGAAATTAACAAAGAGATT 1800
Qy 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAAGATCTGCTTCA 1860
Db 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAAGATCTGCTTCA 1860
Qy 1861 AAAAGAAAGCTGAACCTTAATAGCAGATTAAGCAATATGAACTCGAAATTAATATCC 1920
Db 1861 AAAAGAAAGCTGAACCTTAATAGCAGATTAAGCAATATGAACTCGAAATTAATATCC 1920
Qy 1921 ACAATTCAAAAGACCTTAATAAGATAGGCTGAGGAGAAAGTCTTACCGAGCATATTC 1980
Db 1921 ACAATTCAAAAGACCTTAATAAGATAGGCTGAGGAGAAAGTCTTACCGAGCATATTC 1980
Qy 1981 ATGCGCTTGAATAGTAGTAGTGAATCTAAGCCCACTTAATGTAATGCAATTC 2040
Db 1981 ATGCGCTTGAATAGTAGTAGTGAATCTAAGCCCACTTAATGTAATGCAATTC 2040
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAGTACCAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAGTACCAACCAATGCCAGTCA 2100
Qy 2101 GGCACAGCAGAAACCTTAACATCATGGAAGTAAAGAACTCGAACTGAGCCCAAGAA 2160
Db 2101 GGCACAGCAGAAACCTTAACATCATGGAAGTAAAGAACTCGAACTGAGCCCAAGAA 2160
Qy 2161 GTTACAGCCAAATGAAAGACAGACAAAGTAAAGACATGACAGTATCTTCCAGAGCTG 2220
Db 2161 GTTACAGCCAAATGAAAGACAGACAAAGTAAAGACATGACAGTATCTTCCAGAGCTG 2220
Qy 2221 AGTTAACAAATGACACCTGCTGTTCTTTAATAAGTTCCTAATACAGTGAATTAAGAA 2280
Db 2221 AGTTAACAAATGACACCTGCTGTTCTTTAATAAGTTCCTAATACAGTGAATTAAGAA 2280
Qy 2281 TTGTCATCTTACCTTCCAGAGAAAGAAAAAGAAAGAACTAGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCATCTTACCTTCCAGAGAAAGAAAAAGAAAGAACTAGAAACAGTTAAAGTGT 2340
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAACTG 2400
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTTCAGAACTG 2400
Qy 2401 AAAAGATCTGAGAGTAGAGATTAATCACTGGTACCTGTAATTAAGCACTCAG 2460
Db 2401 AAAAGATCTGAGAGTAGAGATTAATCACTGGTACCTGTAATTAAGCACTCAG 2460
Qy 2461 AAAAGATCTGAGAGTAGAGATTAATCACTGGTACCTGTAATTAAGCACTCAG 2520
Db 2461 AAAAGATCTGAGAGTAGAGATTAATCACTGGTACCTGTAATTAAGCACTCAG 2520
Qy 2521 GTGTGAGTCAAGTGTGAGCATTTGAAAAACCCCAAGGAGCTAATTCATGTTTCCAAAG 2580
Db 2521 GTGTGAGTCAAGTGTGAGCATTTGAAAAACCCCAAGGAGCTAATTCATGTTTCCAAAG 2580
Qy 2581 ATTAATGAATGACACAGAAAGGCTTTAAGTATCATTTGGGACATGAAGTTAACCAAGTC 2640
Db 2581 ATTAATGAATGACACAGAAAGGCTTTAAGTATCATTTGGGACATGAAGTTAACCAAGTC 2640
Qy 2641 GGGAAACAAGCATAAGAAATGAGAAAGTGAATCTGATGCTGATTTTGCAGAAATACAT 2700
Db 2641 GGGAAACAAGCATAAGAAATGAGAAAGTGAATCTGATGCTGATTTTGCAGAAATACAT 2700
Qy 2701 TCAAGGTTTCAAGGCCAGTCAATTTGCTGTTTCAATCAGGAAATGAGAGAG 2760
Db 2701 TCAAGGTTTCAAGGCCAGTCAATTTGCTGTTTCAATCAGGAAATGAGAGAG 2760
Qy 2761 AATGTCGAACATTTCTGCCCACCTGGGTCTTTAAAGAAACAAGTCCAAAGTCACTT 2820

Db 2761 AATGTCGAACATTTCTGCCCACTCTGGGTCTTTAAAGAAACAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTAACAAAAGAGAAAGAAATCAAGAAAGAAATAGTCTAATCAAGCCGTAC 2880
Db 2821 TTGAATGTAACAAAAGAGAAAGAAATCAAGAAAGAAATAGTCTAATCAAGCCGTAC 2880
Qy 2881 AGACAGTAAATATCACTGAGGCTTCCGTGGTGTGAGAAAGATTAAGCCAGTGAAT 2940
Db 2881 AGACAGTAAATATCACTGAGGCTTCCGTGGTGTGAGAAAGATTAAGCCAGTGAAT 2940
Qy 2941 ATGCCAAATGATATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000
Db 2941 ATGCCAAATGATATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTTCAAGGCA 3000
Qy 3001 ACAGAACTGAGCTCAATCTCCAAATAACATGACCTTTTACAAACCCATATCCTATAC 3060
Db 3001 ACAGAACTGAGCTCAATCTCCAAATAACATGACCTTTTACAAACCCATATCCTATAC 3060
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAAGAAATAATCTGCTAGAG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAATGTAAGAAATAATCTGCTAGAG 3120
Qy 3121 AAAACTTTAGAGAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGACATTCGA 3180
Db 3121 AAAACTTTAGAGAACATTCATGTCACCTGAAAGAGAAATGGGAAATGAGACATTCGA 3180
Qy 3181 GTTACGTGAGCAATTTACCCGTAATTAACATTAAGAAATGTTTAAAGAGCCAGCT 3240
Db 3181 GTTACGTGAGCAATTTACCCGTAATTAACATTAAGAAATGTTTAAAGAGCCAGCT 3240
Qy 3241 CAAGCAATTTAATGAAAGTAGGTTCCAGTACTAATGAATGGGCTCAGTATTAATGA 3300
Db 3241 CAAGCAATTTAATGAAAGTAGGTTCCAGTACTAATGAATGGGCTCAGTATTAATGA 3300
Qy 3301 TAGGTTCCAGTATGAAAATTCAGAGCAGAACTAGTGAAGAAACAGAGGCCAAATTTGA 3360
Db 3301 TAGGTTCCAGTATGAAAATTCAGAGCAGAACTAGTGAAGAAACAGAGGCCAAATTTGA 3360
Qy 3361 ATGCTATGCTTATGATTAAGGGGTTTTCGAACTGAGAGCTAATAACAAATCTTCCGGA 3420
Db 3361 ATGCTATGCTTATGATTAAGGGGTTTTCGAACTGAGAGCTAATAACAAATCTTCCGGA 3420
Qy 3421 GTTAATTTGAAGATCCTGAAATTAAGAAAGCAAGAAATATGAAGAGTTCAGACTGTA 3480
Db 3421 GTTAATTTGAAGATCCTGAAATTAAGAAAGCAAGAAATATGAAGAGTTCAGACTGTA 3480
Qy 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAATCAAGACCTATGAGGAAGTATGTC 3540
Db 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAATCAAGACCTATGAGGAAGTATGTC 3540
Qy 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAATGATGTTGTAATTAAG 3600
Db 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAATGATGTTGTAATTAAG 3600
Qy 3601 AAGATATGATTTTCTGAAATGACATTAAGAAAGTCTGCTGTTTAAACAAAGG 3660
Db 3601 AAGATATGATTTTCTGAAATGACATTAAGAAAGTCTGCTGTTTAAACAAAGG 3660
Qy 3661 TCCAGAGAGAGAGCTTACAGAGAGTCTAGCCCTTTTACCAACATCAATTTGGCTCAG 3720
Db 3661 TCCAGAGAGAGAGCTTACAGAGAGTCTAGCCCTTTTACCAACATCAATTTGGCTCAG 3720
Qy 3721 GTTACCGAAGAGAGGAGCAAGAAATTAAGTCTCAGAAAGAACTTAATCTAGAGAGAG 3780
Db 3721 GTTACCGAAGAGAGGAGCAAGAAATTAAGTCTCAGAAAGAACTTAATCTAGAGAGAG 3780
Qy 3781 AAGACCTTCCCTGCTTCCAAACATTTGTAATTTGTAAGTAACAATATACCTTCTCAGT 3840
Db 3781 AAGACCTTCCCTGCTTCCAAACATTTGTAATTTGTAAGTAACAATATACCTTCTCAGT 3840
Qy 3841 CTACTAGGATAGCACCGTTGCTACAGAGTGTCTGTTAAGAAACAGAGAGAAATTTAT 3900
Db 3841 CTACTAGGATAGCACCGTTGCTACAGAGTGTCTGTTAAGAAACAGAGAGAAATTTAT 3900

COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-3

Query Match 99.8%; Score 5701.4; DB 1; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCGACACGAGCTGTGGGTTCTCAGATACTGGGC 60
DB 1 AGCTGCTGAGACTTCTGAGACCCGACACGAGCTGTGGGTTCTCAGATACTGGGC 60

QY 61 CTGCGCTCAGAGAGGCTTCACTCTGCTCTGAGGTAAGTTGATGGAACAGAAAGAA 120
DB 61 CTGCGCTCAGAGAGGCTTCACTCTGCTCTGAGGTAAGTTGATGGAACAGAAAGAA 120

QY 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATGCAAGAA 180
DB 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATGCAAGAA 180

QY 181 TCTTAGAGTGTCCCATCTGCTGAGAGTGTATCAAGAACCTGCTCCCAAGATGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTGCTGAGAGTGTATCAAGAACCTGCTCCCAAGATGTGACC 240

QY 241 ACATATTTTGGCAATTTTGGCATGCTGAAACTTCTCAACAGAAAGAGGCTTTCACAGT 300
DB 241 ACATATTTTGGCAATTTTGGCATGCTGAAACTTCTCAACAGAAAGAGGCTTTCACAGT 300

QY 301 GTCTTTATGTAGAGTATGATATACCAAAAGAGCTTACAGAAAGTATGAGATTTAGTC 360
DB 301 GTCTTTATGTAGAGTATGATATACCAAAAGAGCTTACAGAAAGTATGAGATTTAGTC 360

QY 361 AACTGTTGAAGAGTATGAAATCATTTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420
DB 361 AACTGTTGAAGAGTATGAAATCATTTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420

QY 421 ATGCAAAACAGCTATATTTTGGCAAAAGAGAAATATCTCTCTGAAACATCTAAAGATG 480
DB 421 ATGCAAAACAGCTATATTTTGGCAAAAGAGAAATATCTCTCTGAAACATCTAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGATAGGGCTACAGAAACCGTGCAGAAAGAACTTTTCAAGATG 540
DB 481 AAGTTTCTATCATCCAAAGATAGGGCTACAGAAACCGTGCAGAAAGAACTTTTCAAGATG 540

QY 541 AACCCGAAATCTCTTCTTCCAGAGAAACAGTCTCAGTGTCCAACTCTTAACCTTGAA 600
DB 541 AACCCGAAATCTCTTCTTCCAGAGAAACAGTCTCAGTGTCCAACTCTTAACCTTGAA 600

QY 601 CTGTGAGAACTCTGAGACAAAGCAGCGGATACAACTTCAAAAAGAGCTGTCTTACATG 660
DB 601 CTGTGAGAACTCTGAGACAAAGCAGCGGATACAACTTCAAAAAGAGCTGTCTTACATG 660

QY 661 AATTGGAGTCTGATTTCTTGAAGATACGGTTAATTAAGCACTTATTCAGAGTGGAG 720
DB 661 AATTGGAGTCTGATTTCTTGAAGATACGGTTAATTAAGCACTTATTCAGAGTGGAG 720

QY 721 ATCAAAATTTTACAAATCACCCCTCAAGAAACAGGATGAATCAGTTGGATTCTG 780
DB 721 ATCAAAATTTTACAAATCACCCCTCAAGAAACAGGATGAATCAGTTGGATTCTG 780

QY 781 CAAAAAAGCTGCTGTGTAATTTTCTGAGACGAGTGAACAAATCTGAACATCATCAAC 840
DB 781 CAAAAAAGCTGCTGTGTAATTTTCTGAGACGAGTGAACAAATCTGAACATCATCAAC 840

QY 841 CCAGTAATATGATTTTGAACACCACTGAGAAAGCTGACAGGATCCAGAAAGT 900
DB 841 CCAGTAATATGATTTTGAACACCACTGAGAAAGCTGACAGGATCCAGAAAGT 900

QY 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGAGCATGTGGCAAAATCTCATGCCA 960
DB 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGAGCATGTGGCAAAATCTCATGCCA 960

QY 961 GCTCATTTACAGATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGATGAAA 1020
DB 961 GCTCATTTACAGATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGATGAAA 1020

QY 1021 AGGCTGAATTTCTGATATTAAGCAACAGCTGCTTACAGAGACCAATCAATAGAT 1080
DB 1021 AGGCTGAATTTCTGATATTAAGCAACAGCTGCTTACAGAGACCAATCAATAGAT 1080

QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGAGTCCAGACAGAAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGAGTCCAGACAGAAAAAAGGTAG 1140

QY 1141 ATCTGAATCTGATCCCTGCTGTGAGAGAAAGATGAAATAGCAGAAACTGCTATGCT 1200
DB 1141 ATCTGAATCTGATCCCTGCTGTGAGAGAAAGATGAAATAGCAGAAACTGCTATGCT 1200

QY 1201 CAGAGAACTCTGAGATATGAGAGTGTCTGATTAACATTAATACAGATTCACA 1260
DB 1201 CAGAGAACTCTGAGATATGAGAGTGTCTGATTAACATTAATACAGATTCACA 1260

QY 1261 AAGTTAATGATGTTTCCAGAAAGTATGATGATGTTAGGTTCTGATGACTCATGATG 1320
DB 1261 AAGTTAATGATGTTTCCAGAAAGTATGATGATGTTAGGTTCTGATGACTCATGATG 1320

QY 1321 GGGAGTCTGAATCAAAATGCAAGAGTATGATGATGATGATGATGATGATGATG 1380
DB 1321 GGGAGTCTGAATCAAAATGCAAGAGTATGATGATGATGATGATGATGATGATGATG 1380

QY 1381 AATATTCTGCTTCTTCAAGAAATGATGATGATGATGATGATGATGATGATGATG 1440
DB 1381 AATATTCTGCTTCTTCAAGAAATGATGATGATGATGATGATGATGATGATGATG 1440

QY 1441 TATGTAAAGTAAAGAGTGTCACTCAATCATGATGATGATGATGATGATGATGATG 1500
DB 1441 TATGTAAAGTAAAGAGTGTCACTCAATCATGATGATGATGATGATGATGATGATG 1500

QY 1501 TTGGGAAAACTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 TTGGGAAAACTATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560

QY 1561 TAATTTATGAGACATTTTGTATCTGAGCCCAATATATTAAGAGAGAGAGAGAGAG 1620
DB 1561 TAATTTATGAGACATTTTGTATCTGAGCCCAATATATTAAGAGAGAGAGAGAGAG 1620

QY 1621 AATTAAAGCGTAAAG 1680

Db	1621	AATTAAACGTTAAAGAGACCTTACATCAGGCTTTCATCTGAGGATTTTATCAAAG	1680
Oy	1681	CAGATTTTGGCAGTTTCAAAAAGACTCCTGAATATGATTAATCAGGGAATTAACCAACGAGC	1740
Db	1681	CAGATTTTGGCAGTTTCAAAAAGACTCCTGAATATGATTAATCAGGGAATTAACCAACGAGC	1740
Oy	1741	AGATGTGTCAGTGTGAATTTACTTAATAGTGTCTATGAGATTAACAAAGGTGATT	1800
Db	1741	AGATGTGTCAGTGTGAATTTACTTAATAGTGTCTATGAGATTTAAACAAAGGTGATT	1800
Oy	1801	CTATTCAAAATGAGAAAAATCCTAACATATGATTCATGAGAAACAAATCTGCTTCA	1860
Db	1801	CTATTCAAAATGAGAAAAATCCTAACATATGATTCATGAGAAACAAATCTGCTTCA	1860
Oy	1861	AAACGAAAGCTGAACTTAATAGCAGCAGTATTAAGCAATATGGAATCTCAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACTTAATAGCAGCAGTATTAAGCAATATGGAATCTCAATTAATATCC	1920
Oy	1921	ACAAATTCAAAAGCAGCTTAAAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGATATTC	1980
Db	1921	ACAAATTCAAAAGCAGCTTAAAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGATATTC	1980
Oy	1981	ATGCGCTTGAACTTAATAGTGTGAATTTCTAAAGCCCATTAATTTGTACTGAATTTGCAA	2040
Db	1981	ATGCGCTTGAACTTAATAGTGTGAATTTCTAAAGCCCATTAATTTGTACTGAATTTGCAA	2040
Oy	2041	TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGATACCAACCAATGCGACATCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAAGATACCAACCAATGCGACATCA	2100
Oy	2101	GGCAGCAGCAAACTTACACTCATGGAAGTTAAAGAACTTGCAACTGAGCCCAAGAA	2160
Db	2101	GGCAGCAGCAAACTTACACTCATGGAAGTTAAAGAACTTGCAACTGAGCCCAAGAA	2160
Oy	2161	GTAACAACCCAAATGAACAGCAATTAAGAACATGAGATGATCTTTCCACAGCTGA	2220
Db	2161	GTAACAACCCAAATGAACAGCAATTAAGAACATGAGATGATCTTTCCACAGCTGA	2220
Oy	2221	AGTTAAACAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACACAGTAACTTAAAGAT	2280
Db	2221	AGTTAAACAATGCACTGCTGTTCTTTTACTAAGTGTTCAAATACACAGTAACTTAAAGAT	2280
Oy	2281	TTGTCAATCTTAGCCTTCCAAAGAGAAAAAGAGAAAACTAGAAAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTTAGCCTTCCAAAGAGAAAAAGAGAAAACTAGAAAACAGTTAAAGTGT	2340
Oy	2341	CTAATTAATGCTGGAACCCCAAGATCTCATGTTAAGTGAAGGAGGGTTTTGCAAACTG	2400
Db	2341	CTAATTAATGCTGGAACCCCAAGATCTCATGTTAAGTGAAGGAGGGTTTTGCAAACTG	2400
Oy	2401	AAAGATCTGTAGAGATGACAGTATTTTCACTGTAACCTGTAACGTAATATGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGATGACAGTATTTTCACTGTAACCTGTAACGTAATATGCACTCAGG	2460
Oy	2461	AAAAGTATCTGTTACTGGAAGTTAGCAGCTTAGGGAGGCAAAAAACAGAACCAATTAAT	2520
Db	2461	AAAAGTATCTGTTACTGGAAGTTAGCAGCTTAGGGAGGCAAAAAACAGAACCAATTAAT	2520
Oy	2521	GTTGAGATCAGTGTGACAGATTTTGAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG	2580
Db	2521	GTTGAGATCAGTGTGACAGATTTTGAAAACCCCAAGGACTAATTCATGTTGTTCCAAAG	2580
Oy	2581	ATAATATGAAATGACACAGAGGCTTTAAGTATCTCAATGGGACATGAATTTAAACACAGTC	2640
Db	2581	ATAATATGAAATGACACAGAGGCTTTAAGTATCTCAATGGGACATGAATTTAAACACAGTC	2640
Oy	2641	GGGAAACAAGCATAGAAAATGGAAGAAAGTGAACCTTGAATGCTCAGTATTTGCAGATATCAT	2700
Db	2641	GGGAAACAAGCATAGAAAATGGAAGAAAGTGAACCTTGAATGCTCAGTATTTGCAGATATCAT	2700
Oy	2701	TCAAGTTTCAAGGCGCAGTATTTGCTGTGTTTCAATTCAGGAAATGACAGAGAGG	2760
Db	2701	TCAAGTTTCAAGGCGCAGTATTTGCTGTGTTTCAATTCAGGAAATGACAGAGAGG	2760

Db	2701	TCAGGTTCCAAAGCCGACGTCATTGCTCTGTTTCCAAATCCAGAAATGCAAGAG	2760
QY	2761	AATGCAACATTCCTCTGCCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGCAACATTCCTCTGCCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGAATGTGAACAAAGGAAAGAAATCAGGAAAGAAATGAGTCTAAATATCAGGCTGAC	2880
Db	2821	TTGAATGTGAACAAAGGAAAGAAATCAGGAAAGAAATGAGTCTAAATATCAGGCTGAC	2880
QY	2881	AGACAGTTAATATCACTGACGAGCTTTCTGCTGGTGTGATCAGAAAGATPAAGCCATTGATA	2940
Db	2881	AGACAGTTAATATCACTGACGAGCTTTCTGCTGGTGTGATCAGAAAGATPAAGCCATTGATA	2940
QY	2941	ATGCCAAATGTAGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAAGTTCAGAGCA	3000
Db	2941	ATGCCAAATGTAGATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAAGTTCAGAGCA	3000
QY	3001	ACGAAACTGGAGCTCATTAATCTCCAAATTAACATGGAATTTTACAAACCCCATATGCTATAC	3060
Db	3001	ACGAAACTGGAGCTCATTAATCTCCAAATTAACATGGAATTTTACAAACCCCATATGCTATAC	3060
QY	3061	CACCACTTTTCCCATCAAGTCATTTGTTTAAATGAATGTAAACAAAAATCTGCTAGAG	3120
Db	3061	CACCACTTTTCCCATCAAGTCATTTGTTTAAATGAATGTAAACAAAAATCTGCTAGAG	3120
QY	3121	AAAACTTTAGAGAACTTCAATGTCACCTGACCTGAAGAGAAATGGAAATGAGAACATTTCAA	3180
Db	3121	AAAACTTTAGAGAACTTCAATGTCACCTGACCTGAAGAGAAATGGAAATGAGAACATTTCAA	3180
QY	3181	GTAACGTAGACAACTTAGCCGTAAATACATTAAGAGAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTAACGTAGACAACTTAGCCGTAAATACATTAAGAGAAATGTTTTTAAAGAGCCAGCT	3240
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QY	3601	AAGATCTCAGAGTTGTTCTGAGACACCTGATGACCTGTAGATGATGGTAAATAAG	3660
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QY	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTTAGCCCTTTCAACCATACATTTGGCTCAGG	3720
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QY	3781	AAGAGCTTCCCTGCTCCACACACTTGTTATTTGGTAAAGTAAACAAATATCCTTCTAGT	3840
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DB 5701 GCCCACTACTGA 5711

RESULT 9
US-08-825-487A-3
Sequence 3, Application US/08825487A
Patent No. 6048689
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue., N.W.
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,487A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/060002
FILING DATE: 26-Mar-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 05371, 0012, 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME: 17
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-3

Query Match 99.8%; Score 5701.4; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 3961 AGGAACATCACCTTAGTGAGAAACAAATGTTCTAGCTGTTTCTTCAACAGTGA 4020
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Db 5701 GCCACTACTGA 5711

RESULT 10
US-09-074-476-5
; Sequence 5, Application US/09074476
; Patent No. 6130322
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antoinette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Citez, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Thunder, Denise
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene

NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om13)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-5

Query Match 99.8%; Score 5701.4; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTCTTCAACCAATGCCCCAGATCACTG 5460
D 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTCTTCAACCAATGCCCCAGATCACTG 5460
QY 5461 AATGATGATGACAGCTGTGCTCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 5520
D 5461 AATGATGATGACAGCTGTGCTCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 5520
QY 5521 GCAAGAGGTCACACCAATTTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
D 5521 GCAAGAGGTCACACCAATTTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580
QY 5581 TCCATGCAATTTGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
D 5581 TCCATGCAATTTGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5640
QY 5641 GTGTAGCATCTTACCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
D 5641 GTGTAGCATCTTACCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
QY 5701 GGCACACTGA 5711
D 5701 GGCACACTGA 5711

RESULT 11
US-08-658-322-1
; Sequence 1, Application US/08658322
; Patent No. 5869245
; GENERAL INFORMATION:
; APPLICANT: Yeung, Anthony T.
; TITLE OF INVENTION: Mismatch Endonuclease And Its Use in

Db	481	AAAGTTTCATCATCCAAAGTATGGGCTACAGAAACCCGGCCAAAAGACTTCTACAGAGT	540
Oy	541	AAACCGAAAATCTCTTCTTGACAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA	600
Db	541	AAACCGAAAATCTCTTCTTGACAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA	600
Oy	601	CTGTGAGAACTCTGAGGACAAAGCAGGGGATACAACTCAAAAGACGCTGTCTACATTG	660
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGGGGATACAACTCAAAAGACGCTGTCTACATTG	660
Oy	661	AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTGCAGTGTGGAG	720
Db	661	AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAAGCACTTATTGCAGTGTGGAG	720
Oy	721	ATCAAGATTTGTTCAAATCAACCCCTCAAGAACACAGGAGTAATACATTGTGATTTGTG	780
Db	721	ATCAAGATTTGTTCAAATCAACCCCTCAAGAACACAGGAGTAATACATTGTGATTTGTG	780
Oy	781	CAAAAAGGCGCTGTGTAATTTCTGTGAGCGAGTGTAACTAAATCTGAACATCATCAAC	840
Db	781	CAAAAAGGCGCTGTGTAATTTCTGTGAGCGAGTGTAACTAAATCTGAACATCATCAAC	840
Oy	841	CCAGTAAATGATGATTTGAACACCACTGAGAAAGCGTGACGCTGAGAGGCATTCAGAAAAGT	900
Db	841	CCAGTAAATGATGATTTGAACACCACTGAGAAAGCGTGACGCTGAGAGGCATTCAGAAAAGT	900
Oy	901	ATCAGGGGAGTTCCTTTCAAACTTGCACTGTGGAGCCATGTGGCAAAATCTCATGGCA	960
Db	901	ATCAGGGGAGTTCCTTTCAAACTTGCACTGTGGAGCCATGTGGCAAAATCTCATGGCA	960
Oy	961	GCTCATTTACACATAGAACAGCAGTTTATTAATCACTAAAGACAGATGATGTAGAAA	1020
Db	961	GCTCATTTACACATAGAACAGCAGTTTATTAATCACTAAAGACAGATGATGTAGAAA	1020

Db 1021 AGCGTGAATTCTGTATAAAGCAAACAGCCTTGCTTGGCAAGAGCCAAATACAGAT 1080

Db	1081	GGGCTGGAGTAAGGAAACATGTATGATAGCGGACTCCAGACAGAAAAAAAAGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGGAAAAAGATGGAATAGCAGAAACTGCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGGAAAAAGATGGAATAGCAGAAACTGCCATGCT	1200
QY	1201	CAGAGAACTCAGAGATACGTAGAAGTGTCCCTGGATTAACACTAAATGACAGACTTCAGA	1260
Db	1201	CAGAGAACTCAGAGATACGTAGAAGTGTCCCTGGATTAACACTAAATGACAGACTTCAGA	1260
QY	1261	AAGTTAATAGTAGTGTTTTCCAGAAAGTAGAAGCTTAAAGTTCTGATGACTCACAATGATG	1320
Db	1261	AAGTTAATAGTAGTGTTTTCCAGAAAGTAGAAGCTTAAAGTTCTGATGACTCACAATGATG	1320
QY	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAGCTTCAATAGAGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAGCTTCAATAGAGTAGATG	1380
QY	1381	AATAATTCGTGATCTTCAGAGAAATAGACTTACTGCGCAGATGCTCATGAGGCTTTAA	1440
Db	1381	AATAATTCGTGATCTTCAGAGAAATAGACTTACTGCGCAGATGCTCATGAGGCTTTAA	1440
QY	1441	TATGTAAAAAGTGAAGAAGTTCACTCCAAATCAGTAGAGAGTAATATGGAGACAAAATAT	1500
Db	1441	TATGTAAAAAGTGAAGAAGTTCACTCCAAATCAGTAGAGAGTAATATGGAGACAAAATAT	1500
QY	1501	TTGGGAAAACTATGCGAAGAGCCAGCTCCCACTTAAGCCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACTATGCGAAGAGCCAGCTCCCACTTAAGCCATGTAACTGAAAATC	1560
QY	1561	TAAATTATAGGAGCAATTTGTTACTAGAGCCACAGATTAATAAAGAGAGTCCCTCACAAATA	1620
Db	1561	TAAATTATAGGAGCAATTTGTTACTAGAGCCACAGATTAATAAAGAGAGTCCCTCACAAATA	1620

QY 1621 AATTAAGCGTAAAGAGAGCTACATCAGGCTTCATCTCGAGATTTTATCAAGAAG 1680
 DB 1621 AATTAAGCGTAAAGAGAGAGCTACATCAGGCTTCATCTCGAGATTTTATCAAGAAG 1680
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 DB 1681 CAGATTTGGCAGATTCAAAAGACTCTCGAAATGATTAATCAGGAACTAACCAAGAGC 1740
 QY 1741 AGAATGCTCAAGTGAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1800
 DB 1741 AGAATGCTCAAGTGAATGATTAATGATGATGATGATGATGATGATGATGATGATGAT 1800
 QY 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGATCTGCTTTCA 1860
 DB 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGATCTGCTTTCA 1860
 QY 1861 AAACGAAGCTGAACCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920
 DB 1861 AAACGAAGCTGAACCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920
 QY 1921 ACAATTCAAAG 1980
 DB 1921 ACAATTCAAAG 1980
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 DB 1981 ATGCGCTTGAACCTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
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 DB 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAGAAAAAGTCAACCAATATCCAGTCA 2100
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 DB 2101 GGCACAGCAGAAACCTCACTCATGAGAGTAAAGAACTGGAATCTGAGAGCCAAAGAA 2160
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 DB 2161 GTAAACAGCCAAATGAG 2220
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 DB 2281 TTGTCATCTGACCTTCCAG 2340
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 DB 2641 GGGAAACAGAGATAG 2700

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 DB 2881 AGACAGTTAATATCACTGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
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 DB 3121 AAAACCTTTGAG 3180
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 DB 3541 ATGATCTCAGGTTGTTCTGAG 3600
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 QY 3661 TTCAG 3720
 DB 3661 TTCAG 3720
 QY 3721 GTTACGAG 3780
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 QY 3781 AAGAGCTTCCGCTGCTTCCAG 3840
 DB 3781 AAGAGCTTCCGCTGCTTCCAG 3840

Db 3781 AAGAGCTTCCGCTTCCAGACTGTATTTGGTAAGTAACAATATACCTTCAGT 3840
Qy 3841 CTACTAGGCTATGACCCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGGAAATTTAT 3900
Db 3841 CTACTAGGCTATGACCCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGGAAATTTAT 3900
Qy 3901 TATCATTAAGAAATAGCTTAATTAAGTACGTACAGGTAAATTAATGAGGAAAGGCTTC 3960
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Qy 3961 AGGAACATCACCTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
Db 3961 AGGAACATCACCTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020
Qy 4021 GTGAATTGGAAGACTTGAAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4080
Db 4021 GTGAATTGGAAGACTTGAAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4080
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Db 4081 CCAAAACAATGAGGATCAGTCTGAAGCCAGGAGTTGCTGAGTGAACAAGATTTGG 4140
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Qy 4201 TGGATTTCAAACCTTAGTGAAGACAGCATCTGGGTGTGAAGTGAACAAACCTCTGGAAG 4260
Db 4201 TGGATTTCAAACCTTAGTGAAGACAGCATCTGGGTGTGAAGTGAACAAACCTCTGGAAG 4260
Qy 4261 ACTGCTCAGGGCTATCTCTCAGATGATGATTTAAACCACTCAGCAGAGGAGTACCATGC 4320
Db 4261 ACTGCTCAGGGCTATCTCTCAGATGATGATTTAAACCACTCAGCAGAGGAGTACCATGC 4320
Qy 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGCTGAATTAAGAGCTGTGTTGAACAC 4380
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGCTGAATTAAGAGCTGTGTTGAACAC 4380
Qy 4381 ATGGAGCAGGCTTCTAAGACGCTACCTTCATCATTAAGTGAATCTGCTGCTGAGG 4440
Db 4381 ATGGAGCAGGCTTCTAAGACGCTACCTTCATCATTAAGTGAATCTGCTGCTGAGG 4440
Qy 4441 ACCTGCGAAATCCAGAACCAACACATCAGAAAAAGCATTTAATCTTACAGAAAAAGTA 4500
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Qy 4501 GTGAATACCTTAATTAAGCAGAAATCCAGAGGCTTTCTGCTGAACAAGTTGAGTGTCTG 4560
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Qy 4561 CAGATAGTCTTACCGATAAATAAAGAAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620
Db 4561 CAGATAGTCTTACCGATAAATAAAGAAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620
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Db 4621 GCCCATCATTAAGATAGTGTGTATCATATGACAGTTGCTCTGAGAGTCTTCAAGATAGAA 4680
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Qy 4741 AGTGGGGCCACAGATTTGAAGGAAACATCTTACTGTCAGAGGCAAGATCTAGAGGGAA 4800
Db 4741 AGTGGGGCCACAGATTTGAAGGAAACATCTTACTGTCAGAGGCAAGATCTAGAGGGAA 4800
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGATCTGATCTCTTCTG 4860
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCCCTGATCTGATCTCTTCTG 4860
Qy 4861 AAGACAGAGCCCAAGTCACTGCTGTTGCAACATCACTTCAACCTTGCATTTGA 4920
Db 4861 AAGACAGAGCCCAAGTCACTGCTGTTGCAACATCACTTCAACCTTGCATTTGA 4920

Db 4861 AAGACAGAGCCCAAGTCACTGCTGTTGCAACATCACTTCAACCTTGCATTTGA 4920
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Db 4921 AAGTCCCCCAATGGAATGTGAGAAATGTCGCCAGGGGTCAGCTGCTCATACTGTG 4980
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Db 4981 ATACTGCTGGGTATTAATCAATGGAAGAAAGTGTGAGCAGGAGAAAGCAGAAATTTGACAG 5040
Qy 5041 CTTCACAGAAAGGCTCAACAAAGATGTCCATGTGTGTCTGCTGCTGACCCCAAG 5100
Db 5041 CTTCACAGAAAGGCTCAACAAAGATGTCCATGTGTGTCTGCTGCTGACCCCAAG 5100
Qy 5101 AATTATCTGTGTGACAAAGTTGCGAGAAACCCATCATCTTAATCTAATCTAATTA 5160
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Qy 5161 CTGAAGACTACTCATGTGTGTATGAAGACAGATGCTGAGTTGTGTGAACGACAC 5220
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Qy 5221 TGAATATTTCTAGAAATTTGGGAGGAAATGGGTAGTTAGTATTTCTGGTGAAC 5280
Db 5221 TGAATATTTCTAGAAATTTGGGAGGAAATGGGTAGTTAGTATTTCTGGTGAAC 5280
Qy 5281 AGCTATTAAGAAAGAAATGCTGAATGAGATGATTTGAATGATGAGAGATGAG 5340
Db 5281 AGCTATTAAGAAAGAAATGCTGAATGAGATGATTTGAATGATGAGAGATGAG 5340
Qy 5341 TCAATGGAAGAAACCAACCAAGGTCGAGAGCAAGAAATCCAGAGCAAGAAAGTCT 5400
Db 5341 TCAATGGAAGAAACCAACCAAGGTCGAGAGCAAGAAATCCAGAGCAAGAAAGTCT 5400
Qy 5401 TGAAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAATGCTCCAGATCACTGG 5460
Db 5401 TGAAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAATGCTCCAGATCACTGG 5460
Qy 5461 AATGATGTGACAGTGTGTGTGCTGTGTGTGAAGAGCTTCAATCACTGCTG 5520
Db 5461 AATGATGTGACAGTGTGTGTGCTGTGTGTGAAGAGCTTCAATCACTGCTG 5520
Qy 5521 GCACAGGTGTCACCAATGTTGTTGTGACGAGATGCTGAGCAGAGACAAATGCT 5580
Db 5521 GCACAGGTGTCACCAATGTTGTTGTGACGAGATGCTGAGCAGAGACAAATGCT 5580
Qy 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGTGGGTGTTGACA 5640
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGTGGGTGTTGACA 5640
Qy 5641 GTGTAGCACTCAACAGTCCAGAGGCTGACACCTGATCCCAATCCCAATCCCA 5700
Db 5641 GTGTAGCACTCAACAGTCCAGAGGCTGACACCTGATCCCAATCCCAATCCCA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 12
US-08-603-753D-1
; Sequence 1, Application US/08603753D
; Patent No. 5691857
GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CSILLA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA1
LOCATION: Genbank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-08-603-753D-1

Query Match 99.8%; Score 5699.8; DB 2; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCGACAGGCTGTGGGTTTCTCAATTAATCTGGCC 60
DB 1 ACTCGCTGAGACTTCTGAGACCCGACAGGCTGTGGGTTTCTCAATTAATCTGGCC 60
QY 61 CCTGGGCTGAGAGGCTTCACTCTGCTGGGTAAGTTCATGGAACGAAAGAA 120
DB 61 CCTGGGCTGAGAGGCTTCACTCTGCTGGGTAAGTTCATGGAACGAAAGAA 120
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DB 361 AACTGTTGAAGACTATGTAATATCATTTGCTTTTCACTTGAACACAGTTGGAGT 420
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RESULT 14
 US-08-986-106-1
 : Sequence 1, Application US/08986106
 : Patent No. 6177410
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: HOLT, JEFFREY T.
 :
 : APPLICANT: JENSEN, ROY A.
 :
 : APPLICANT: KING, MARY-CLAIRE
 :
 : APPLICANT: STERNER, MITCHELL S.

```

1 APPLICANT: ROBINSON-BENION, CHERYL L.
2 APPLICANT: THOMPSON, MARTIN E.
3 TITLE OF INVENTION: THERAPEUTIC METHODS FOR
4 TITLE OF INVENTION: PROSTATE CANCER
5 NUMBER OF SEQUENCES: 26
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: ARLES A. TAYLOR, JR.
8 STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
9 STREET: BOULEVARD
10 CITY: DURHAM
11 STATE: NORTH CAROLINA
12 COUNTRY: USA
13 ZIP: 27707
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
17 COMPUTER: IBM PC/XT/AT compatible
18 OPERATING SYSTEM: Windows 3.1
19 SOFTWARE: WORD PERFECT 6.1 and ASCII
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/986,106
22 FILING DATE:
23 CLASSIFICATION:
24 PRIORITY APPLICATION DATA:
25 APPLICATION NUMBER: 08/603,753
26 FILING DATE: 20 FEB 1996
27 ATTORNEY/AGENT INFORMATION:
28 NAME: ARLES A. TAYLOR, JR.
29 REGISTRATION NUMBER: 39,395
30 REFERENCE/DOCKET NUMBER: 1242/3
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (919) 493-8000
33 TELEFAX: (919) 419-0383
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 5712
37 TYPE: nucleic acid
38 STRANDEDNESS: double
39 TOPOLOGY: linear
40
41 FEATURE:
42 NAME/KEY: BRCA1
43 LOCATION: Genbank accession no. U14680
44 PUBLICATION INFORMATION:
45 AUTHORS: Miki, Y., et. al.
46 TITLE: A strong candidate gene for the breast and
47 TITLE: ovarian cancer susceptibility gene BRCA1.
48 JOURNAL: Science
49 VOLUME: 266
50 PAGES: 66-71
51 DATE: 1994
52
53 US-08-986-106-1
54
55 Query Match 99.8%; Score 5699.8; DB 4; Length 5712;
56 Best Local Similarity 99.9%; Pred. No. 0;
57 Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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 QY 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTGAAATTAATATCC 1920
 Db 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAACTGAAATTAATATCC 1920
 QY 1921 ACAATTCAAAAGCCTTAATAAAGATAGGCTGAGAGAGAGTCTTACAGGATATTC 1980
 Db 1921 ACAATTCAAAAGCCTTAATAAAGATAGGCTGAGAGAGAGTCTTACAGGATATTC 1980
 QY 1981 ATGCGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 Db 1981 ATGCGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 QY 2041 TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAATGCCAGTCA 2100
 Db 2041 TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAATGCCAGTCA 2100
 QY 2101 GGCACAGCAAAACCTCAACATCATGAGAGTAAAGAACTGCACTGAGGCAAGAA 2160
 Db 2101 GGCACAGCAAAACCTCAACATCATGAGAGTAAAGAACTGCACTGAGGCAAGAA 2160
 QY 2161 GTAAAGGCAAAATGAACAGCAAGTAAAGAAAGATGATGATGATGATGATGATGAT 2220
 Db 2161 GTAAAGGCAAAATGAACAGCAAGTAAAGAAAGATGATGATGATGATGATGATGAT 2220
 QY 2221 AGTTAAACAATGACCTGTTCTTTTACTTAAGTGTCAATACCAAGTAAAGAT 2280
 Db 2221 AGTTAAACAATGACCTGTTCTTTTACTTAAGTGTCAATACCAAGTAAAGAT 2280
 QY 2281 TTGTCAATCTGACCTTCCAGAGAAAGAAAGAGAACTTGAACAGTTAAAGTGT 2340
 Db 2281 TTGTCAATCTGACCTTCCAGAGAAAGAAAGAGAACTTGAACAGTTAAAGTGT 2340
 QY 2341 CTAATTAAGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCACAC 2400
 Db 2341 CTAATTAAGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGCACAC 2400
 QY 2401 AAAGATCTGTAGAGATGACAGTATTTCACTGTGATCTGTGATTTGAGCACTGAG 2460
 Db 2401 AAAGATCTGTAGAGATGACAGTATTTCACTGTGATCTGTGATTTGAGCACTGAG 2460
 QY 2461 AAAGATCTGTGATCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 Db 2461 AAAGATCTGTGATCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 QY 2521 GTGTAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
 Db 2521 GTGTAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
 QY 2581 ATTAATGAATGACACAGAGGCTTTAAGTATCAATTGGACATGAAATTAACACAGTC 2640
 Db 2581 ATTAATGAATGACACAGAGGCTTTAAGTATCAATTGGACATGAAATTAACACAGTC 2640
 QY 2641 GGGAAACAAGCTTGAATGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700
 Db 2641 GGGAAACAAGCTTGAATGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2700

Db	3781	AAGAGCTTCCTGCTCCACACTTGTTATTTGGTAAAGTAACATATACCTTCTCACT	3841
Qy	3841	CTACTAGGCATAGACCGGTGCTACCGAGTGTCTGTCTTAAGAACACAGAGGAAATTTAT	3900
Db	3841	CTACTAGGCATAGACCGGTGCTACCGAGTGTCTGTCTTAAGAACACAGAGGAAATTTAT	3900
Qy	3901	TATCATTTGAAGAAATGCTTAAATGATCTGCAGTAACACAGTAAATATTTGGCAAAAGCATCTC	3966
Db	3901	TATCATTTGAAGAAATGCTTAAATGATCTGCAGTAACACAGTAAATATTTGGCAAAAGCATCTC	3966
Qy	3961	AGGAACATCACCTTAGTAGAGGAAACAAATGTTCTGTAGCTTGTTTCTTCACAGTGA	4020
Db	3961	AGGAACATCACCTTAGTAGAGGAAACAAATGTTCTGTAGCTTGTTTCTTCACAGTGA	4020
Qy	4021	GTGAATTGGAAGACTTGACTGCAATACAAACACCAGATCTTTCTTGATTGTTCTT	4086
Db	4021	GTGAATTGGAAGACTTGACTGCAATACAAACACCAGATCTTTCTTGATTGTTCTT	4086
Qy	4081	CCAAACAAATAGAGCATCATGTTCTGAACACGAGGATGTGTCTGATGTAACAAGAAATTTGG	4144
Db	4081	CCAAACAAATAGAGCATCATGTTCTGAACACGAGGATGTGTCTGATGTAACAAGAAATTTGG	4144
Qy	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGCAAGCA	4200
Qy	4201	TGATATTCAACTTAGTGTAAGACAGCATCTGGGTGTGAGATGAAACAAAGCTCTCTGAAG	4266
Db	4201	TGATATTCAACTTAGTGTAAGACAGCATCTGGGTGTGAGATGAAACAAAGCTCTCTGAAG	4266
Qy	4261	ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAACCATCAGACAGGATACCATTC	4322
Db	4261	ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAACCATCAGACAGGATACCATTC	4322
Qy	4321	AACATPAACCTGTATTAAGCTCCAGCAGAAATGGCTGAACCTGAAGCTGTGTGAACACAGC	4388
Db	4321	AACATPAACCTGTATTAAGCTCCAGCAGAAATGGCTGAACCTGAAGCTGTGTGAACACAGC	4388
Qy	4381	ATGGAGGCAGCCTTTCTAACAGCTACCCCTTCATATTAAGTACTCCTCTGCCCTTGAAG	4444
Db	4381	ATGGAGGCAGCCTTTCTAACAGCTACCCCTTCATATTAAGTACTCCTCTGCCCTTGAAG	4444
Qy	4441	ACCTGCGCAATTCAGAACAAAGCACATAGAAAAAGCAGTATTAACCTTCACAGAAAAGTA	4500
Db	4441	ACCTGCGCAATTCAGAACAAAGCACATAGAAAAAGCAGTATTAACCTTCACAGAAAAGTA	4500
Qy	4501	GTGAATACCCATATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAGGTCTTG	4566
Db	4501	GTGAATACCCATATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAGGTCTTG	4566
Qy	4561	CAGATAGTCTTACACAGTAAAAATAAAGAACCCAGAGTGGAAAGTCACTCCCTCTTAAT	4622
Db	4561	CAGATAGTCTTACACAGTAAAAATAAAGAACCCAGAGTGGAAAGTCACTCCCTCTTAAT	4622
Qy	4621	GCCCATCATTAAGATGATAGTGTGTATCATGACAGTGTCTTGAGGAGTCTTCAGAAATAGA	4688
Db	4621	GCCCATCATTAAGATGATAGTGTGTATCATGACAGTGTCTTGAGGAGTCTTCAGAAATAGA	4688
Qy	4681	ACTACCCATTCACAGAGAGCTCATTTAAGTTGTGTGATGTGAGAGCAACAGCTGGAAG	4744
Db	4681	ACTACCCATTCACAGAGAGCTCATTTAAGTTGTGTGATGTGAGAGCAACAGCTGGAAG	4744
Qy	4741	AGTCTGGGCCACACAGATTTGACGAAACATTTACTTTCGCAAGCAATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACAGATTTGACGAAACATTTACTTTCGCAAGCAATCTAGAGGAA	4800
Qy	4801	CCCCTTACCTGGAATCTGGAATCAGCCCTCTCTCTGATGACCCCTGAATCTGATCTCTTG	4866
Db	4801	CCCCTTACCTGGAATCTGGAATCAGCCCTCTCTCTGATGACCCCTGAATCTGATCTCTTG	4866
Qy	4861	AAGACAGAGCCCCAGAGTCACTGTGTGGCAATATCCATCTTCAACCTTCATTTGA	4922
Db	4861	AAGACAGAGCCCCAGAGTCACTGTGTGGCAATATCCATCTTCAACCTTCATTTGA	4922

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